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OM nucleic - nucleic search, using sw model

Run on: September 2, 2004, 13:12:03; Search time 103 Seconds  
(without alignments)  
6513.938 Million cell updates/sec

Title: US-10-087-080-31

Perfect score: 1209  
Sequence: 1 atgaagctggagagctgctgcgt.....tggagagctcctcctagcttga 1209

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Issued Patents NA:\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	6.6	320	4	US-09-833-381-1266
2	25	2.1	1965	4	US-09-220-133-21
3	25	2.1	4695	2	US-08-231-193A-57
4	25	2.1	4695	2	US-08-486-273A-57
5	25	2.1	4695	2	US-08-940-086A-57
6	25	2.1	4695	4	US-08-940-035A-57
7	25	2.1	4695	4	US-08-935-105A-57
8	25	2.1	4695	4	US-09-648-797-57
9	25	2.1	4695	4	US-09-386-123-57
10	24	2.0	159	3	US-09-437-457-11
11	24	2.0	429	4	US-09-641-638-324
12	24	2.0	1860	2	US-08-331-644-3
13	24	2.0	1860	5	PCT-US93-04102-3
14	24	2.0	3387	1	US-08-064-271-11
15	24	2.0	3387	2	US-08-627-254C-29
16	24	2.0	3387	4	US-09-023-655-1050
17	22	1.8	3387	4	US-08-930-589A-19
18	22	1.8	3387	4	US-09-599-781-19
19	20	1.7	480	4	US-09-674-608A-4
20	20	1.7	1454	4	US-09-372-422A-19
21	20	1.7	2561	4	US-09-616-289-48
22	20	1.7	4403765	3	US-09-103-840A-2
23	20	1.7	441529	3	US-09-103-840A-1
24	19	1.6	576	4	US-09-252-991A-13112
25	19	1.6	633	4	US-09-252-991A-12687
26	19	1.6	720	4	US-09-252-991A-2351
27	19	1.6	720	4	US-09-252-991A-2640

c	28	19	1.6	1101	4	US-09-489-039A-2638	Sequence 2638, Ap
c	29	19	1.6	1192	3	US-09-318-448-18	Sequence 18, Appl
c	30	19	1.6	1248	4	US-09-489-039A-6144	Sequence 6144, Appl
c	31	19	1.6	1278	4	US-09-252-991A-2483	Sequence 2483, Ap
c	32	19	1.6	1563	4	US-09-252-991A-2566	Sequence 2566, Ap
c	33	19	1.6	2124	4	US-09-252-991A-12830	Sequence 12830, A
c	34	19	1.6	2634	3	US-08-941-936-1	Sequence 1, Appl
c	35	19	1.6	3623	1	US-08-306-691B-35	Sequence 35, Appl
c	36	19	1.6	43280	2	US-08-804-227C-1	Sequence 1, Appl
c	37	18	1.5	18	2	US-08-627-254C-12	Sequence 12, Appl
c	38	18	1.5	248	4	US-09-397-787-24	Sequence 24, Appl
c	39	18	1.5	420	4	US-09-252-991A-7967	Sequence 7967, Ap
c	40	18	1.5	504	4	US-09-252-991A-9584	Sequence 9584, Ap
c	41	18	1.5	957	4	US-09-252-991A-51	Sequence 51, Appl
c	42	18	1.5	1077	4	US-09-522-714-17	Sequence 17, Appl
c	43	18	1.5	1143	4	US-09-252-991A-5748	Sequence 5748, Ap
c	44	18	1.5	1188	4	US-09-252-991A-5131	Sequence 5131, Ap
c	45	18	1.5	1239	4	US-09-252-991A-9666	Sequence 9666, Ap

## ALIGNMENTS

```
RESULT 1
US-09-833-381-1266
; Sequence 1266, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1266
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(320)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1266

Query Match      6.6%; Score 80; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.4e-24;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 GGACAACTACAGAGCTCAACCCCAAGAGAGTACCTTGGCGAGGGGCTCTCCG 626
Db 1 GGACAACTACAGAGCTCAACCCCAAGAGAGTACCTTGGCGAGGGGCTCTCCG 60

QY 627 CCGCGCCGCAAGCGCTCA 646
Db 61 CCGCGCCGCAAGCGCTCA 80

RESULT 2
US-09-220-132-21
; Sequence 21, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
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PRIOR APPLICATION NUMBER: US 60/068,821  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 191  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 21  
LENGTH: 1965  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-220-132-21

Query Match 2.1%; Score 25; DB 4; Length 1965;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CCTACTCGTACATCGGCTCATCG 382  
DB 196 CCTACTCGTACATCGGCTCATCG 220

RESULT 3  
US-08-231-193A-57  
Sequence 57, Application US/08231193A  
Patent No. 5849895  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,193A  
FILING DATE: 20-APR-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/052,459  
FILING DATE: 20-APR-1993  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 485..4495  
US-08-231-193A-57

Query Match 2.1%; Score 25; DB 2; Length 4695;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGGCGGCGGCGGCGGCGG 309  
DB 3700 GGGGCCAGGCGGCGGCGGCGGCGG 3724

RESULT 4  
US-08-486-273A-57  
Sequence 57, Application US/08486273A  
Patent No. 5985586  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA  
TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,273A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/231,193  
FILING DATE: 20-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-9383B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 485..4495  
US-08-486-273A-57

Query Match 2.1%; Score 25; DB 2; Length 4695;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGGCGGCGGCGGCGGCGG 309  
DB 3700 GGGGCCAGGCGGCGGCGGCGGCGG 3724

RESULT 5  
US-08-940-086A-57  
Sequence 57, Application US/08940086A  
Patent No. 6111091  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen W.  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,086A  
FILING DATE: 29-SEPT-97  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/231,193  
FILING DATE: 20-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/052,449  
FILING DATE: 20-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24735-9383C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 450-8400  
TELEFAX: (619) 450-8499  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 485..4495  
US-08-940-086A-57

Query Match 2.1%; Score 25; DB 3; Length 4695;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGCGCGCGCGCGCGG 309  
DB 3700 GGGGCCAGCGCGCGCGCGCGG 3724

RESULT 6  
US-08-940-035A-57  
Sequence 57, Application US/08940035A  
Patent No. 6316611  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: U.S.A.

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,035A  
FILING DATE: 29-SEPT-97  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/231,193  
FILING DATE: 20-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/052,449  
FILING DATE: 20-APR-1993  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-9383E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 485..4495  
US-08-940-035A-57

Query Match 2.1%; Score 25; DB 4; Length 4695;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGCGCGCGCGCGCGG 309  
DB 3700 GGGGCCAGCGCGCGCGCGCGG 3724

RESULT 7  
US-08-935-105A-57  
Sequence 57, Application US/08935105A  
Patent No. 6376660  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
APPLICANT: Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/935,105A  
FILING DATE: 29-SEPT-97  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/231,193  
FILING DATE: 20-APR-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/052,449  
FILING DATE: 20-APR-1993  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-9383D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 485..4495  
US-08-933-105A-57

Query Match 2.1%; Score 25; DB 4; Length 4695;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGGGCGGGCGGGCGGGG 309  
DB 3700 GGGGCCAGGGCGGGCGGGCGGGG 3724

RESULT 8  
US-09-648-797-57  
Sequence 57, Application US/09648797  
Patent No. 6469142  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
Ellis, Steven B.  
Liew, Chen W.  
Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McAnuliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/648,797  
FILING DATE: 28-Aug-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,086A  
FILING DATE: 29-SEPT-97  
APPLICATION NUMBER: US 08/231,193  
FILING DATE: 20-APR-1994  
APPLICATION NUMBER: US 08/052,449  
FILING DATE: 20-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 2435-9383C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 450-8400  
TELEFAX: (619) 450-8499  
INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 485..4495  
US-09-648-797-57

Query Match 2.1%; Score 25; DB 4; Length 4695;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGGGCCAGGGCGGGCGGGCGGGG 309  
DB 3700 GGGGCCAGGGCGGGCGGGCGGGG 3724

RESULT 9  
US-09-386-123-57  
Sequence 57, Application US/09386123  
Patent No. 6521413  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
Ellis, Steven B.  
Liew, Chen W.  
APPLICANT: Liew, Chen W.  
Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McAnuliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/386,123  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/486,273  
FILING DATE: 06-JUNE-95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/231,193  
FILING DATE: 20-APR-1994  
APPLICATION NUMBER: US 08/052,449  
FILING DATE: 20-APR-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-9383F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-450-8403  
TELEFAX: 858-587-5360  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:





Query Match 2.0%; Score 24; DB 2; Length 1860;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CCTACTCGTACATCGCGCTCATC 381  
Db 759 CCTACTCGTACATCGCGCTCATC 782

RESULT 13  
PCT-US93-04102-3  
Sequence 3, Application PC/TUS9304102  
GENERAL INFORMATION:  
APPLICANT: Tao, Wufan  
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/04102  
FILING DATE: 19930430  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/882,292  
FILING DATE: 13-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41472A-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
TRLEX: 422523 COOP UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1860 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US93-04102-3

Query Match 2.0%; Score 24; DB 5; Length 1860;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CCTACTCGTACATCGCGCTCATC 381  
Db 759 CCTACTCGTACATCGCGCTCATC 782

RESULT 14  
US-08-064-271-11  
Sequence 11, Application US/08064271  
Patent No. 5543297  
GENERAL INFORMATION:  
APPLICANT: Kennedy, Brian P.  
APPLICANT: Cromlish, Manda A.  
APPLICANT: Mancini, Joseph A.  
APPLICANT: O'Neill, Gary  
APPLICANT: Vickers, Philip J.

APPLICANT: Wong, Elizabeth  
TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND  
ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 Lincoln Avenue  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 in, 1.4Kb  
OPERATING SYSTEM: Apple Macintosh  
SOFTWARE: Microsoft Word 5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/064,271  
FILING DATE: 19930506  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Panzer, Curtis C.  
REGISTRATION NUMBER: 33,752  
REFERENCE/DOCKET NUMBER: 189061A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)594-3199  
TELEFAX: (908)594-4720  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3387 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-064-271-11

Query Match 2.0%; Score 24; DB 1; Length 3387;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 890 GCGCGCGCGCTGCGCGCTGC 913  
Db 73 GCGCGCGCGCTGCGCGCTGC 96

RESULT 15  
US-08-627-254C-29  
Sequence 29, Application US/08627254C  
Patent No. 5859229  
GENERAL INFORMATION:  
APPLICANT: Kniss, Douglas A.  
TITLE OF INVENTION: Bicosanoid Formation  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calfee, Halter & Griwold LLP  
STREET: 800 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: USA  
ZIP: 44114

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/627,254C  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Golick, Mary E  
REGISTRATION NUMBER: 34,829  
REFERENCE/DOCKET NUMBER: 18525/00107

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8200
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-627-254C-29

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Query Match      2.0%; Score 24; DB 2; Length 3387;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       73 GGGCGGGGGCTGCGCGCGCTGC 96

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Search completed: September 2, 2004, 15:11:14  
 Job time : 106 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2004, 14:59:04 ; Search time 611 Seconds  
(without alignments)  
9835.521 Million cell updates/sec

Title: US-10-087-080-31

Perfect score: 1209  
Sequence: 1 atgaagcttgagagtgcttcgt.....tggagacgcctcctagctga 1209

Scoring table: Oligo NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3267054 seqs, 2485319735 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

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19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1209	100.0	1209	13	US-10-229-345-9 Sequence 9, Appli
2	1209	100.0	1209	13	US-10-274-177-9 Sequence 9, Appli
3	1209	100.0	1209	17	US-10-087-080-31 Sequence 31, Appli
4	1209	100.0	1209	16	US-10-650-112-9 Sequence 9, Appli
5	923	76.3	1212	17	US-10-650-112-25 Sequence 25, Appli
6	264	21.8	585	13	US-10-027-632-23153 Sequence 23153,
7	264	21.8	585	16	US-10-027-632-23153 Sequence 23153,
8	80	6.6	320	9	US-09-833-381-1266 Sequence 1266, Ap
9	77	6.4	1203	17	US-10-650-112-26 Sequence 26, Appli
10	53	4.4	1203	17	US-10-650-112-27 Sequence 27, Appli
11	53	4.4	1760	12	US-10-152-319A-1814 Sequence 1814, Ap
12	30	2.5	312	15	US-10-029-386-23708 Sequence 23708, A
13	30	2.5	425	13	US-10-027-632-138699 Sequence 138699,
14	30	2.5	425	13	US-10-027-632-138700 Sequence 138700,

15	30	2.5	425	13	US-10-027-632-138701	Sequence 138701,
16	30	2.5	425	13	US-10-027-632-138703	Sequence 138703,
17	30	2.5	425	16	US-10-027-632-138699	Sequence 138699,
18	30	2.5	425	16	US-10-027-632-138700	Sequence 138700,
19	30	2.5	425	16	US-10-027-632-138701	Sequence 138701,
20	30	2.5	425	16	US-10-027-632-138703	Sequence 138703,
21	30	2.5	599	15	US-09-867-701-3098	Sequence 10008, A
22	25	2.1	441	9	US-09-867-701-3098	Sequence 10008, A
23	25	2.1	1335	15	US-10-029-386-20506	Sequence 20506, A
24	25	2.1	1287	10	US-09-960-706-947	Sequence 947, App
25	25	2.1	4695	9	US-09-945-901-57	Sequence 947, App
26	25	2.1	4695	14	US-10-007-747-57	Sequence 57, Appl
27	27	2.1	4695	15	US-10-038-9937-57	Sequence 57, Appl
28	24	2.0	159	9	US-09-929-447-11	Sequence 11, Appl
29	24	2.0	159	9	US-09-437-458-11	Sequence 11, Appl
30	24	2.0	310	16	US-10-393-905-26	Sequence 26, Appl
31	24	2.0	4059	16	US-10-170-097-324	Sequence 324, App
32	24	2.0	1056	15	US-10-101-510-419	Sequence 419, App
33	33	2.0	1979	17	US-10-806-634-3	Sequence 3, Appli
34	24	2.0	2271	15	US-10-101-510-133	Sequence 133, App
35	24	2.0	2487	13	US-10-342-887-1045	Sequence 1045, App
36	24	2.0	2487	13	US-10-172-118-1045	Sequence 1045, App
37	24	2.0	2487	15	US-10-205-823-135	Sequence 135, App
38	24	2.0	2563	14	US-10-044-090-477	Sequence 477, App
39	24	2.0	3387	16	US-10-191-997-87	Sequence 87, Appl
40	24	2.0	3387	17	US-10-641-643-1050	Sequence 1050, App
41	24	2.0	4496	14	US-10-044-090-478	Sequence 478, App
42	24	2.0	4496	14	US-10-071-766-46	Sequence 46, Appl
43	24	2.0	4750	12	US-10-247-671-126	Sequence 126, App
44	24	2.0	5181	15	US-09-968-007A-802	Sequence 802, App
45	24	2.0	11064	10	US-09-949-293-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-10-229-345-9  
Sequence 9, Application US/10229345  
Publication No. US20040038220A1  
GENERAL INFORMATION:  
APPLICANT: MARKOWITZ, Sanford D.  
TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS  
FILE REFERENCE: CWRU-P01-003  
CURRENT APPLICATION NUMBER: US/10/229,345  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 1209  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1161)..(1161)  
OTHER INFORMATION: n=a, c, g, or t  
US-10-229-345-9

Query Match	100.0%	Score 1209;	DB 13;	Length 1209;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1209;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	ATGAAGTTGAGAGTGTTCCTCGCGCGGCGCAACAGGAGGAGTACCTG	60	
DB	1	ATGAAGTTGAGAGTGTTCCTCGCGCGGCGCAACAGGAGGAGTACCTG	60	
QY	61	GAGGCGCGGCGGCGGAGCGCGCGGCGGCGGCGGCGGCGGAGAGTCCCTG	120	
DB	61	GAGGCGCGGCGGCGGAGCGCGCGGCGGCGGCGGCGGCGGAGAGTCCCTG	120	
QY	121	GGCTCAGATGGAGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGAGATGCGAG	180	
DB	121	GGCTCAGATGGAGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGAGATGCGAG	180	

QY	18	GGCGACGGCGAAACGAGTGGCGGAGGCGCGGCGCGCGCGCGAGGAGGCGATCCGCGCAGCA	240
Db	181	GGCGACGGCGAAACGAGTGGCGGAGGCGCGGCGCGCGCGAGGAGGCGATCCGCGCAGCA	240
QY	241	GCTGCTGACGCGGTGGTGGCGGAGGCGCGGAGCGCGGAGCGCGGAGCGCGGCGCGGCG	300
Db	241	GCTGCTGACGCGGTGGTGGCGGAGGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGCG	300
QY	301	GGCGCGGGGAGACGGCGAGAGGGTGCACGACGAAGCGCATTAAGCGCGCGGCCCAAGCCCCC	360
Db	301	GGCGCGGGGAGACGGCGAGAGGGTGCACGACGAAGCGCATTAAGCGCGCGGCCCAAGCCCCC	360
QY	361	TACTGTATCATCGCGCTCATCGCCATGCGCATTCGCGCATCTGGCGGAGCGGCGCTTGAAG	420
Db	361	TACTGTATCATCGCGCTCATCGCCATGCGCATTCGCGCATCTGGCGGAGCGGCGCTTGAAG	420
QY	421	CTGGCGGAGATCAACAGATCTCATAGGGGCAAGTATCCCTTTTTCGCGGAGGTACAAG	480
Db	421	CTGGCGGAGATCAACAGATCTCATAGGGGCAAGTATCCCTTTTTCGCGGAGGTACAAG	480
QY	481	GGCTGGSCAACTCGTGCAGCGCACAACTTTTCGCTCAACGACTGCTTGTCAAGTGTG	540
Db	481	GGCTGGSCAACTCGTGCAGCGCACAACTTTTCGCTCAACGACTGCTTGTCAAGTGTG	540
QY	541	CGCGACCCCTTCGCGGCGCTGGGAGCAAGGACAACTACTGATGTCTAACCCCAACAGGAG	600
Db	541	CGCGACCCCTTCGCGGCGCTGGGAGCAAGGACAACTACTGATGTCTAACCCCAACAGGAG	600
QY	601	TACACCTTTCGCGCGAGGGGTCTTCGCGCGCGCGCGCGCAAGCGCTCAGCGCACGCGCGCG	660
Db	601	TACACCTTTCGCGCGAGGGGTCTTCGCGCGCGCGCGCGCAAGCGCTCAGCGCACGCGCGCG	660
QY	661	GTCCCGCGCGCGCGGCTGGCGCGGAGGAGCGCCCGGAGCTTCCCGCGCGCGCGCGCG	720
Db	661	GTCCCGCGCGCGCGGCTGGCGCGGAGGAGCGCCCGGAGCTTCCCGCGCGCGCGCGCGCG	720
QY	721	GCGCGCGCGCGCGCGGCTGGCGCGCGGATGGGCTGGCGCGCGCGCGCGCGCGCGCGCGCG	780
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QY	781	AGCCCGCGGAGCAATTTCTCAGACTCTTGCGCATGCAACAGATCTTGCAGAGCCCTTC	840
Db	781	AGCCCGCGGAGCAATTTCTCAGACTCTTGCGCATGCAACAGATCTTGCAGAGCCCTTC	840
QY	841	CGACGCCCTCGCTCTAGGAGACACGCGCGCGCGCGGAGACAGCTTCAAGTGGAGCGCGCGCG	900
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QY	901	TGCCCGCGCGCTTCGCGCGCTTCCCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCG	960
Db	901	TGCCCGCGCGCTTCGCGCGCTTCCCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCG	960
QY	961	CGGCTCTGGCGGTACGGCGCGGAGCGAGCGCGGAGCTGGCGCGCGCGGAGGCGGAGGTTG	1020
Db	961	CGGCTCTGGCGGTACGGCGCGGAGCGAGCGCGGAGCTGGCGCGCGCGGAGGCGGAGGTTG	1020
QY	1021	CGACCGACCGCGCGCGCGCTCTGCTTGCATCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCAAGCGCA	1080
Db	1021	CGACCGACCGCGCGCGCGCTCTGCTTGCATCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCAAGCGCA	1080
QY	1081	CTCGAGAGCGCGCGCGCGCGCGGAGCGAGACCTGTACTCGCCCTTCGCGCTGGCGCGCACGC	1140
Db	1081	CTCGAGAGCGCGCGCGCGCGCGGAGCGAGACCTGTACTCGCCCTTCGCGCTGGCGCGCACGC	1140
QY	1141	CTGCAAGCGGCGCTTATGTCCAGCGTCTTGCGCGCGCATCTGTGTAACCGGTGAGACGCTTC	1200
Db	1141	CTGCAAGCGGCGCTTATGTCCAGCGTCTTGCGCGCGCATCTGTGTAACCGGTGAGACGCTTC	1200
QY	1201	CTAAGCTTGA	1209
Db	1201	CTAAGCTTGA	1209

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RESULT 2
US-10-274-177-9
; Sequence 9, Application US/10274177
; Publication No. US20040038225A1
; GENERAL INFORMATION:
; APPLICANT: NARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; FILE REFERENCE: CWRU-P01-003
; CURRENT APPLICATION NUMBER: US/10/274.177
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/10/229,345
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1161)..(1161)
; OTHER INFORMATION: n=a, c, g, or t
US-10-274-177-9

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[illegible]

[illegible]

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1 RESULT 3
2 US-10-087-080-31
3 ; Sequence 31, Application US/10087080
4 ; Publication No. US20030235820A1
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Mack, David H.
7 ; APPLICANT: Markowitz, Sanford David
8 ; APPLICANT: Eos Biotechnology, Inc.
9 ; APPLICANT: Case Western Reserve University
10 ; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal
11 ; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
12 ; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
13 ; FILE REFERENCE: 018501-000840US
14 ; CURRENT APPLICATION NUMBER: US/10/087,080
15 ; CURRENT FILING DATE: 2002-10-25
16 ; PRIOR APPLICATION NUMBER: US 60/272,206
17 ; PRIOR FILING DATE: 2001-02-27
18 ; PRIOR APPLICATION NUMBER: US 60/281,149
19 ; PRIOR FILING DATE: 2001-04-02
20 ; PRIOR APPLICATION NUMBER: US 60/284,555
21 ; PRIOR FILING DATE: 2001-04-17
22 ; NUMBER OF SEQ ID NOS: 41
23 ; SOFTWARE: PatentIn Ver. 2.1
24 ; SEQ ID NO 31
25 ; LENGTH: 1209
26 ; TYPE: DNA
27 ; ORGANISM: Homo sapiens
28 ; FEATURE:
29 ; OTHER INFORMATION: winged helix/forkhead transcription factor (HFFH1)
30 ; FEATURE:
31 ; NAME/KEY: modified_base
32 ; LOCATION: (1161)

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OTHER INFORMATION: n = g, a, c or t  
US-10-087-080-31

Query Match	100.0%;	Score 1209;	DB 16;	Length 1209;
Best Local Similarity	100.0%;	Pred. Nc. 0;		
Matches 1209;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGAAGTTGAGAGGTTGTCCTCCCTCGCGCGGCGCCACGGAGACAACACGGGCGATACCTG	60
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QY	61	GAGGAGCGCGGCGGAGCGCGCGCTCCCGCTGTGCGCGCGGAGACGACCTCCCTG	120
Db	61	GAGGAGCGCGGCGGAGCGCGCGCTCCCGCTGTGCGCGCGGAGACGACCTCCCTG	120
QY	121	GGCTCAGATGGGGACTGCGCGGCGCCAAAGCTTCCGTGGGCGGCGGCGCAAGATTACGACG	180
Db	121	GGCTCAGATGGGGACTGCGCGGCGCCAAAGCTTCCGTGGGCGGCGGCGCAAGATTACGACG	180
QY	181	GGCGACGCGCAACAGAGTGCGGGAGGCGGCGCGGCGGAGAGAGGCATCCCGGACAGA	240
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QY	301	GGCGCGGAGAGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGCGGCGG	360
Db	301	GGCGCGGAGAGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGCGG	360
QY	361	TACTCGTACATCGCGCTCATCGCCATGCGCATCCGCGACTCGCGCGGCGGCGCTTGAAG	420
Db	361	TACTCGTACATCGCGCTCATCGCCATGCGCATCCGCGACTCGCGCGGCGGCGCTTGAAG	420
QY	421	CTGGCGGAGATTCACAGAGTACCTCATATGGGAGAGTTCCCTTTTCCGGGCGAGCTACACG	480
Db	421	CTGGCGGAGATTCACAGAGTACCTCATATGGGAGAGTTCCCTTTTCCGGGCGAGCTACACG	480
QY	481	GAGTGGCGCACTCCGTGCGCCACCAACTTTCGCTCAACGACTGCTTCGTCAAGATGCTG	540
Db	481	GAGTGGCGCACTCCGTGCGCCACCAACTTTCGCTCAACGACTGCTTCGTCAAGATGCTG	540
QY	541	CGGACCCCTCTCGGCGCCTTGGGGCAAGACACTACTGATGCTCAACCCCAACGACGAG	600
Db	541	CGGACCCCTCTCGGCGCCTTGGGGCAAGACACTACTGATGCTCAACCCCAACGACGAG	600
QY	601	TACACCTTCGCGACGAGGAGTCTTCGCGCGCGCGCGCAAGGAGGCTCAGACACCGGCGCG	660
Db	601	TACACCTTCGCGACGAGGAGTCTTCGCGCGCGCGCGCAAGGAGGCTCAGACACCGGCGCG	660
QY	661	GTCCCGCGCGCGGAGCTGCGGCGCGCGCGCGAGAGGAGCCCGGAGCTCCCGCGCGCGCGCG	720
Db	661	GTCCCGCGCGCGGAGCTGCGGCGCGCGCGCGAGAGGAGCCCGGAGCTCCCGCGCGCGCGCG	720
QY	721	GGCGCGGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	780
Db	721	GGCGCGGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	780
QY	781	AGCGCGCGGCGCAAGTTCTTCAGACTCTTCCTTCGCAATCAGACAGACTCTGCGCAAGCCCTTC	840
Db	781	AGCGCGCGGCGCAAGTTCTTCAGACTCTTCCTTCGCAATCAGACAGACTCTGCGCAAGCCCTTC	840
QY	841	CGAGAGCGTGTGCTCAGAGGACACAGGCGCCCGGAGACGACGCTTCAGTGTGGGCGCGCGCG	900
Db	841	CGAGAGCGTGTGCTCAGAGGACACAGGCGCCCGGAGACGACGCTTCAGTGTGGGCGCGCGCG	900
QY	901	TGCGCGCGCGTGCCTCCGCGCTCTCCCGCGCTCTCCCGCGCGCGCGCGCGCGCGCGCTG	960
Db	901	TGCGCGCGCGTGCCTCCGCGCTCTCCCGCGCTCTCCCGCGCGCGCGCGCGCGCGCGCTG	960
QY	961	CGGCTTGGCGGTAAGGCGCGGAGCGCGGCGCGGCGCGGCGCGCGCGCGCGCGCGGAGCTG	1020

Db	961	CGCGTCTGCGCGTACGAGGCGGGGAGCGAGCGGCGCGCTGCGGCGCGCGCGAGGCGCAGAGGTG	1020
QY	1021	CCACCGACCGGCGCGCGCCCTCTCTGCTTGCACCTCTCCCGGCGGGGAGCCCCCGCCAAAGCCA	1080
Db	1021	CCACCGACCGGCGCGCGCCCTCTCTGCTTGCACCTCTCCCGGCGGGGAGCCCCCGCCAAAGCCA	1080
QY	1081	CTCCGAGGCGCGGCGGCGCGGCGGACCTGTACTGCGCCCTCGCGGCGCTGCGCCGAGCC	1140
Db	1081	CTCCGAGGCGCGGCGGCGCGGCGGCGGACCTGTACTGCGCCCTCGCGGCGCTGCGCCGAGCC	1140
QY	1141	CTGCGAGGCGGCGCTTGTCTCGGCGTCTTGCGCCCGGCACTGTGTTACCCCGGTGAGAGAGCTTC	1200
Db	1141	CTGCGAGGCGGCGCTTGTCTCGGCGTCTTGCGCCCGGCACTGTGTTACCCCGGTGAGAGAGCTTC	1200
QY	1201	CTAGCTTGA	1209
Db	1201	CTAGCTTGA	1209

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RESULT 4
US-10-650-112-9
; Sequence 9, Application US/10650112
; Publication No. US20040110712A1
; Publication No. US20040110712A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CWRU-P01-04
; CURRENT APPLICATION NUMBER: US/10/650,112
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1161)..(1161)
; OTHER INFORMATION: n is a,t,g or c
US-10-650-112-9

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Query Match	100.0%;	Score 1209;	DB 17;	Length 1209;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1209; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ATGAAGTTGAGAGTGTTCCTCCCTCGCGCGGCGCCACGAGGAGCAAGAGCGAGTGAACCTG 60

Db 1 ATGAAGTTGAGAGTGTTCCTCCCTCGCGCGGCGCCACGAGGAGCAAGAGCGAGTGAACCTG 60

QY 61 GAGGGCGCGGGCGGCGACGAGCGCGCTCCCTGCTCTCGAGCGCGGAGACGACTCTCCCTG 120

Db 61 GAGGGCGCGGGCGGCGACGAGCGCGCTCCCTGCTCTCGAGCGCGGAGACGACTCTCCCTG 120

QY 121 GGCTCAGATGAGGGGACTGCGCGCGGCGCAAGCGGTCGCGGGGCGGCGGCGCCAGAGTACGAG 180

Db 121 GGCTCAGATGAGGGGACTGCGCGCGGCGCAAGCGGTCGCGGGGCGGCGGCGCCAGAGTACGAG 180

QY 181 GCGCAGCGCGGAAACAGAGTCCGGAGGAGCGCGGAGCGCGGAGAGGCGCATCCCGCGAGCA 240

Db 181 GCGCAGCGCGGAAACAGAGTCCGGAGGAGCGCGGAGCGCGGAGAGGCGCATCCCGCGAGCA 240

QY 241 GCTGCTGCAACGAGTGGCTGGCGAGGAGCGCGAGGCGCGGAGCGCGGAGCGCGGAGCGCGGCG 300

Db 241 GCTGCTGCAACGAGTGGCTGGCGAGGAGCGCGAGGCGCGGAGCGCGGAGCGCGGAGCGCGGCG 300

QY 301 GGCGCGGAGAGCGCGAGGAGTGCACGACAGACCATTAACGCGCGGCGCCCAAGCCCCCCC 360

Db	301	GGCGCGGGAGACGGGCGAGGGGTGACGACGAGCAAGCGCATATATACGGGGCGGGCCCAAGCCCCC	360
QY	361	TACTGTATCATCGCGCTCATATGCCATATGGCCATTCGCGCATCTGGGGGGCGGGCGCTTATGAC	420
Db	361	TACTGTATCATCGCGCTCATATGCCATATGGCCATTCGCGCATCTGGGGGGCGGGCGCTTATGAC	420
QY	421	CTGGCGGAGATTCACAGAGTATCTCATATGGGCAAGTTCCTTTTTCGGCGGAGCTACACG	480
Db	421	CTGGCGGAGATTCACAGAGTATCTCATATGGGCAAGTTCCTTTTTCGGCGGAGCTACACG	480
QY	481	GGCTGAGGCACTCCGTGCGCCACAACCTTTCGTCTCAACGACTGCTTGTCAAGGTGCTG	540
Db	481	GGCTGAGGCACTCCGTGCGCCACAACCTTTCGTCTCAACGACTGCTTGTCAAGGTGCTG	540
QY	541	CGCGACCCCTTGCGGAGCTCTGGGGCAAGGACATATCTGATGCTACATCCCAACGCGAG	600
Db	541	CGCGACCCCTTGCGGAGCTCTGGGGCAAGGACATATCTGATGCTACATCCCAACGCGAG	600
QY	601	TACACCTTCCGCGACGAGGGCTTTCGCGCGCGCGCAAGCGCTCAGCGACCGCGCGCG	660
Db	601	TACACCTTCCGCGACGAGGGCTTTCGCGCGCGCGCAAGCGCTCAGCGACCGCGCGCG	660
QY	661	GTCCCGCGCCGAGCTGCGGCGCGAGAGGCCCCGAGGCTTCCCGCGCCCGCGCGCTC	720
Db	661	GTCCCGCGCCGAGCTGCGGCGCGAGAGGCCCCGAGGCTTCCCGCGCCCGCGCGCTC	720
QY	721	GCGCGCGCGCCCCGGGCGCTCGGCCCGCATGCGCTGCGCCCGCGCGCAAGAGAGAGGGCGCC	780
Db	721	GCGCGCGCGCCCCGGGCGCTCGGCCCGCATGCGCTGCGCCCGCGCGCAAGAGAGAGGGCGCC	780
QY	781	AGCCCCGGGGCAAGTTCTCCAGCTCCTTGCGCATGCGACAGCATCTGCGCAAGCGCTTTC	840
Db	781	AGCCCCGGGGCAAGTTCTCCAGCTCCTTGCGCATGCGACAGCATCTGCGCAAGCGCTTTC	840
QY	841	CGCAGCCGTCGCGCTCAGGAGACAGGCGCCCGGAGACGAGCTTCAATGGGGCGCGCGCCC	900
Db	841	CGCAGCCGTCGCGCTCAGGAGACAGGCGCCCGGAGACGAGCTTCAATGGGGCGCGCGCCC	900
QY	901	TGCCCGCGCTGCGCGCGCTTCCCGCGCGCTCTCTCCCGCGGCGCTCTGCAAGGCGCTGCTG	960
Db	901	TGCCCGCGCTGCGCGCGCTTCCCGCGCGCTCTCTCCCGCGGCGCTCTGCAAGGCGCTGCTG	960
QY	961	CGGCTCTGCGCTAAGGCGCGGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGAGGCGGAGGTG	1020
Db	961	CGGCTCTGCGCTAAGGCGCGGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGAGGCGGAGGTG	1020
QY	1021	CCACCGACCGGCGCGCCCTCTGCTTGTGACCTTCCCGGCGGCGGCGCCCGCCCAAGCCA	1080
Db	1021	CCACCGACCGGCGCGCCCTCTGCTTGTGACCTTCCCGGCGGCGGCGCCCGCCCAAGCCA	1080
QY	1081	CTCCGAGGCGCGGCGCGCGCGGCGGCGGCGGCACTGTATGCTGCTGCGGCTGCGCGGAGCC	1140
Db	1081	CTCCGAGGCGCGGCGCGCGCGGCGGCGGCGGCACTGTATGCTGCTGCGGCTGCGCGGAGCC	1140
QY	1141	CTGCGAGGCGGCTTATGCTCCGAGCTCTTGCCCGCGGACCTGTGCTACCCCGGTGAGACGCTC	1200
Db	1141	CTGCGAGGCGGCTTATGCTCCGAGCTCTTGCCCGCGGACCTGTGCTACCCCGGTGAGACGCTC	1200
QY	1201	CTAGCTTGA 1209	
Db	1201	CTAGCTTGA 1209	

```

RESULT 5
US-10-650-112-25
; Sequence 25, Application US/10650:12
; Publication No. US20040110712A1
;
; GENERAL INFORMATION:
; APPLICANT: MARKOMITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CWRU-P01-04
; CURRENT APPLICATION NUMBER: US/10/650, 112
; CURRENT FILING DATE: 2003-08-26
;

```



PRIOR APPLICATION NUMBER: 10/274,177  
PRIOR FILING DATE: 2002-10-18  
PRIOR APPLICATION NUMBER: 10/229,245  
PRIOR FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBER: 60/406,296  
PRIOR FILING DATE: 2002-08-27  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 25  
LENGTH: 1212  
TYPE: DNA  
ORGANISM: HUMAN FOXO1  
US-10-650-112-25

Query Match 76.3%; Score 923; DB 17; Length 1212;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 180 GGGCGACGGCGAACAAGATGCGGAGCGCGCGCGAGAGCGATCCCGCAGC 239  
DB 183 GGGCGACGGCGAACAAGATGCGGAGCGCGCGCGAGAGCGATCCCGCAGC 242  
QY 240 AGCTGTGAGCGGTGTGGCGGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 299  
DB 243 AGCTGTGAGCGGTGTGGCGGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 302  
QY 300 CGGCGCGGAGCGCGAGCGGTGCAAGCAAGCATATACGCGCGCGCGCGCGCG 359  
DB 303 CGGCGCGGAGCGCGAGCGGTGCAAGCAAGCATATACGCGCGCGCGCGCGCG 362  
QY 360 CTAATGTATATGCGCTATGCGCATGCGCATGCGCATGCGCGCGCGCGCGCT 419  
DB 363 CTAATGTATATGCGCTATGCGCATGCGCATGCGCATGCGCGCGCGCGCGCT 422  
QY 420 GGTGGGAGGATCAAGATCACTGAGGCAAGTTCCTTTTCCGCGGACTACAC 479  
DB 423 GGTGGGAGGATCAAGATCACTGAGGCAAGTTCCTTTTCCGCGGACTACAC 482  
QY 480 GGGCTGGGCAACTCCGTGCGCCACCAACTTTCGCTCAAGAGTGTGCTAAGGT 539  
DB 483 GGGCTGGGCAACTCCGTGCGCCACCAACTTTCGCTCAAGAGTGTGCTAAGGT 542  
QY 540 GGGCGAATCCCTGCGCGCGCTGCGGCAAGCAACTGATGCTCAACCCCAAGCG 599  
DB 543 GGGCGAATCCCTGCGCGCGCTGCGGCAAGCAACTGATGCTCAACCCCAAGCG 602  
QY 600 GTACACCTTGGCGAGCGGGGTCTTCCGCGCGCGCGCGCGCGCGCGCGCG 659  
DB 603 GTACACCTTGGCGAGGGGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCG 662  
QY 660 GGTCCCG 719  
DB 663 GGTCCCG 722  
QY 720 CGGCG 779  
DB 723 CGGCG 782  
QY 780 CAGCCCG 839  
DB 783 CAGCCCG 842  
QY 840 CGGAGCGGTGCGCTCAGGAGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 899  
DB 843 CGGAGCGGTGCGCTCAGGAGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 902  
QY 900 CTGCG 959  
DB 903 CTGCG 962  
QY 960 GCGCGCTGCGCGGTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1019  
DB 963 GCGCGCTGCGCGGTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1022

QY 1020 GCCACCGACCG 1079  
DB 1023 GCCACCGACCG 1082  
QY 1080 ACTCCGAGGCG 1139  
DB 1083 ACTCCGAGGCG 1142  
QY 1140 CCTGCAAGCGCGCT 1153  
DB 1143 CCTGCAAGCGCGCT 1156

## RESULT 6

US-10-027-632-231353/c  
Sequence 231353, Application US/10027632  
Publication No. US20020198371A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT FILING DATE: 2002-04-30  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 231353  
TYPE: DNA  
LENGTH: 585  
ORGANISM: Human  
US-10-027-632-231353

Query Match 21.8%; Score 264; DB 13; Length 585;  
Best Local Similarity 99.5%; Pred. No. 1,9e-115;  
Matches 364; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 788 CGGCGAAGTTCGACGCTCTTTCGCGATGACAGATCTTGGCGAAGCCCTTCCGAGCG 847  
DB 585 CGGCGAAGTTCGACGCTCTTTCGCGATGACAGATCTTGGCGAAGCCCTTCCGAGCG 526  
QY 848 GTGCGCTCAGGAGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 907  
DB 525 GCGCGCTCAGGAGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 466  
QY 908 CGCTCCCGCGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967  
DB 465 CGCTCCCGCGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 406  
QY 968 GCGCGTAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027  
DB 405 GCGCGTAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 346  
QY 1028 CGGCG 1087  
DB 345 CGGCG 286  
QY 1088 GCG 1147

Db 285 GCCCGGCGCGCGCGCGCGCACTGTGACCTGCCCCCTGGCGGTGCGCGAGACCCCTGACAG 226  
QY 1148 CGGCT 1153  
Db 225 CGGCT 220

## RESULT 7

US-10-027-632-231353/C  
; Sequence 231353, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108927.129  
; CURRENT APPLICATION NUMBER: US/10/027, 632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231353  
; LENGTH: 585  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-231353

Query Match 21.8%; Score 264; DB 16; Length 585;  
Best Local Similarity 99.5%; Pred. No. 1.9e-115;  
Matches 364; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 788 CGGCGAGTCTCTCAGCTCTTGGCCATCGACATCTCGGCAAGCCCTTCCGACGCC 847  
Db 585 CGGCGAAGTCTCTCAGCTCTTGGCCATCGACATCTCGGCAAGCCCTTCCGACGCC 526  
QY 848 GTCGCTCAGGAGACAGCGCCCGCGAGAGAGCTTCAAGTGGGCGCGCGCTTCCCGC 907  
Db 525 GCGGCTCAGGAGACAGCGCCCGCGAGAGAGCTTCAAGTGGGCGCGCGCTTCCCGC 466  
QY 908 CGTGGCCGCGCTTCCCGCGCTCTCTCCCGCGCGCGCTTCAAGGCGCTTGTGCGGCTCT 967  
Db 465 CGTGGCCGCGCTTCCCGCGCTCTCTCCCGCGCGCGCTTCAAGGCGCTTGTGCGGCTCT 406  
QY 968 GCGGCTCAGGAGAGCGCGCGAGCGCGGCTGGGCGCGCGAGAGTGGACCGA 1027  
Db 405 GCGGCTCAGGAGAGCGCGCGAGCGCGGCTGGGCGCGCGAGAGTGGACCGA 346  
QY 1028 CGGCGCGCGCTCTCTGCTTCACTCTCCCGCGCGCGCGCGCGCAAGCACTCCGAG 1087  
Db 345 CGGCGCGCGCTCTCTGCTTCACTCTCCCGCGCGCGCGCGCGCAAGCACTCCGAG 286  
QY 1088 GCGCGCGCGCGCGCGCGAGAGCTTCAAGTGGGCGCGCGCTTCCCGAGCTTCCAGG 1147  
Db 285 GCGCGCGCGCGCGCGCGAGAGCTTCAAGTGGGCGCGCGCTTCCCGAGCTTCCAGG 226  
QY 1148 CGGCT 1153  
Db 225 CGGCT 220

## RESULT 8

US-09-833-381-1266  
; Sequence 1266, Application US/09833381  
; Patent No. US20020132090A1  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. US20020132090A1 Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1266  
; LENGTH: 320  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(320)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-1266

Query Match 6.6%; Score 80; DB 9; Length 320;  
Best Local Similarity 100.0%; Pred. No. 6.8e-28;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 GGAACAATCTGATGTCTCAACCCCAACGCGATACCTTGGCGAGGGGTCTTCCG 626  
Db 1 GGAACAATCTGATGTCTCAACCCCAACGCGATACCTTGGCGAGGGGTCTTCCG 60  
QY 627 CCGCGCGCGAGCGCTCA 646  
Db 61 CCGCGCGCGAGCGCTCA 80

## RESULT 9

US-10-650-112-26  
; Sequence 26, Application US/10650112  
; Publication No. US20040110712A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKOWITZ, Sanford D.  
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS  
; FILE REFERENCE: CWRU-P01-044  
; CURRENT APPLICATION NUMBER: US/10/650,112  
; PRIOR FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 10/274,177  
; PRIOR FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 10/229,245  
; PRIOR FILING DATE: 2002-08-26  
; PRIOR APPLICATION NUMBER: 60/406,296  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; LENGTH: 1203  
; TYPE: DNA  
; ORGANISM: MOUSE FOXO1  
US-10-650-112-26

Query Match 6.4%; Score 77; DB 17; Length 1203;  
Best Local Similarity 99.2%; Pred. No. 1.4e-26;  
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 526 TTGCTCAAGTGTGCGCGACCTCTCGCGGCTTGGGCGAAGGCACTACTGATGCTC 585  
Db 517 TTGCTCAAGTGTGCGCGACCTCTCGCGGCTTGGGCGAAGGCACTACTGATGCTC 576  
QY 586 AACCCAAAGCGAGTACCTTGGCGAGAGGGTCTTTCGCGCGCGCGCGAGCGCTC 645  
Db 577 AACCCAAAGCGAGTACCTTGGCGAGAGGGTCTTTCGCGCGCGCGCGAGCGCTC 636

Qy 646 AGCCACCG 653  
DB 637 AGCCACCG 644

## RESULT 10

US-10-650-112-27  
; Sequence 27, Application US/10650112  
; Publication No. US20040110712A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKOWITZ, Sanford D.  
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS  
; FILE REFERENCE: CMRU-P01-044  
; CURRENT APPLICATION NUMBER: US/10/650,112  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 10/274,177  
; PRIOR FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 10/229,245  
; PRIOR FILING DATE: 2002-08-26  
; PRIOR APPLICATION NUMBER: 60/406,296  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 1203  
; TYPE: DNA  
; ORGANISM: RAT FOXQ1  
US-10-650-112-27

Query Match 4.4%; Score 53; DB 17; Length 1203;  
Best Local Similarity 100.0%; Pred. No. 3.6e-15;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 601 TACACCTTCGCCGACGGGGTCTTCGCCGCCGCCGACGAGCGCTCAGCCACCG 653  
DB 592 TACACCTTCGCCGACGGGGTCTTCGCCGCCGCCGACGAGCGCTCAGCCACCG 644

## RESULT 11

US-10-152-319A-1814  
; Sequence 1814, Application US/10152319A  
; Publication No. US20040072160A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgs, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Blashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/10/152,319A  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/330,462  
; PRIOR FILING DATE: 2001-10-22

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2221  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1814  
; LENGTH: 1760  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. NM\_022858  
US-10-152-319A-1814

Query Match 4.4%; Score 53; DB 12; Length 1760;  
Best Local Similarity 100.0%; Pred. No. 3.3e-15;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 601 TACACCTTCGCCGACGGGGTCTTCGCCGCCGCCGACGAGCGCTCAGCCACCG 653  
DB 796 TACACCTTCGCCGACGGGGTCTTCGCCGCCGCCGACGAGCGCTCAGCCACCG 848

## RESULT 12

US-10-029-386-23708  
; Sequence 23708, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: AEOmica-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 23708  
; LENGTH: 312  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR2.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5  
; OTHER INFORMATION: SWISSPROT HIT: Q60688, EVALU 1.00e-58  
; OTHER INFORMATION: EST HUMAN HIT: AW236501.1, EVALU 3.00e-76  
; OTHER INFORMATION: NT HIT: U13223.1, EVALU 0.00e+00  
US-10-029-386-23708

Query Match 2.5%; Score 30; DB 15; Length 312;  
Best Local Similarity 100.0%; Pred. No. 0.00041;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 AAGCCCCCTACTGTGATACGGCGCTCATC 381  
DB 11 AAGCCCCCTACTGTGATACGGCGCTCATC 40

## RESULT 13

US-10-027-632-138699  
; Sequence 138699, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.139  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12

```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 138699
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-138699
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Query Match
Best Local Similarity 100.0%; Score 30; DB 13; Length 425;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 352 AAGCCCCCTACTCGTACATCGGCGTCATC 381
DB 91 AAGCCCCCTACTCGTACATCGGCGTCATC 120
```

```
RESULT 14
US-10-027-632-138700
; Sequence 138700, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 138700
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-138700
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Query Match
Best Local Similarity 100.0%; Score 30; DB 13; Length 425;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 91 AAGCCCCCTACTCGTACATCGGCGTCATC 120
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RESULT 15
US-10-027-632-138701
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; Sequence 138701, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 138701
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-138701
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Query Match
Best Local Similarity 100.0%; Score 30; DB 13; Length 425;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 352 AAGCCCCCTACTCGTACATCGGCGTCATC 381
DB 91 AAGCCCCCTACTCGTACATCGGCGTCATC 120
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Search completed: September 2, 2004, 16:44:57
Job time : 612 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 27, 2004, 15:18:23 ; Search time 31.5 Seconds

(without alignments)  
3962.908 Million cell updates/sec

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Sequence: 1 atgaagcttgagagctgttcgt.....tggagacgcctcctagctga 1209

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FEATEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents AA:

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3: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	431.5	19.7	553	3	US-09-083-351-2
2	431.5	19.7	553	3	US-09-083-352-2
3	394.5	18.0	330	4	US-09-083-352-12
4	387	17.7	473	3	US-09-976-594-928
5	347	15.9	480	1	US-08-857-076-99
6	347	15.9	480	1	US-07-882-292-2
7	347	15.9	480	5	US-08-331-644-2
8	336	15.3	347	3	PCT/US93-04102-2
9	333	15.2	106	3	US-08-857-076-100
10	333	15.2	106	3	US-09-083-351-14
11	332	15.2	106	3	US-09-083-352-14
12	332	15.2	106	3	US-09-083-351-15
					US-09-083-352-15

13	329	15.0	544	4	US-09-087-134-14	Sequence 14, Appl
14	320.5	14.6	106	3	US-09-083-351-12	Sequence 12, Appl
15	320.5	14.6	106	3	US-09-083-352-12	Sequence 12, Appl
16	320.5	14.6	2294	4	US-09-252-991A-1231	Sequence 17231, A
17	319	14.6	365	3	US-09-113-309-2	Sequence 2, Appl1
18	319	14.6	365	3	US-09-521-109-2	Sequence 2, Appl1
19	319	14.6	365	4	US-09-252-991A-25394	Sequence 25394, A
20	317	14.5	369	4	US-09-252-991A-10843	Sequence 30843, A
21	315	14.4	663	4	US-09-083-351-13	Sequence 13, Appl
22	314.5	14.4	106	3	US-09-083-352-13	Sequence 13, Appl
23	314.5	14.4	106	3	US-09-252-991A-18035	Sequence 18035, A
24	312.5	14.3	783	4	US-09-252-991A-20509	Sequence 20509, A
25	311.5	14.2	863	4	US-09-252-991A-26068	Sequence 26068, A
26	311	14.2	638	4	US-09-252-991A-20668	Sequence 20668, A
27	307	14.0	957	4	US-09-252-991A-20408	Sequence 20408, A
28	307	14.0	1706	4	US-09-083-351-7	Sequence 31760, A
29	307	14.0	106	3	US-09-083-351-7	Sequence 7, Appl1
30	305.5	14.0	106	3	US-09-083-352-7	Sequence 11, Appl
31	305.5	14.0	534	4	US-09-113-309-19	Sequence 27110, A
32	304.5	13.9	518	3	US-09-521-109-19	Sequence 19, Appl
33	304.5	13.9	518	3	US-09-562-332-19	Sequence 19, Appl
34	304.5	13.9	518	4	US-09-252-991A-18296	Sequence 18296, A
35	304.5	13.8	467	4	US-09-252-991A-24514	Sequence 24514, A
36	303	13.8	720	4	US-09-252-991A-21881	Sequence 21881, A
37	303	13.8	726	4	US-09-252-991A-20675	Sequence 20675, A
38	303	13.8	904	4	US-09-976-594-615	Sequence 615, App
39	302.5	13.8	904	4	US-09-370-838-187	Sequence 187, App
40	302.5	13.8	904	4	US-09-252-991A-18296	Sequence 18296, A
41	302	13.8	904	4	US-09-252-991A-18296	Sequence 18296, A
42	301.5	13.4	809	4	US-09-252-991A-18296	Sequence 18296, A
43	297.5	13.2	467	4	US-09-252-991A-31949	Sequence 31949, A
44	296.5	13.5	495	4	US-09-252-991A-31949	Sequence 31949, A
45	296.5	13.5	495	4	US-09-252-991A-31949	Sequence 31949, A

#### ALIGNMENTS

RESULT 1  
US-09-083-351-2  
; Sequence 2, Application US/09083351  
; Patent No. 6087107  
; GENERAL INFORMATION:  
; APPLICANT: Sheffield, Val C.  
; APPLICANT: Alward, Wallace L.M.  
; APPLICANT: Stone, Edwin M.  
; APPLICANT: Nishimura, Darryl  
; APPLICANT: Patel, Shiva  
; TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR  
; TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HONG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/083,351  
; FILING DATE: 22-MAY-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: UTA-029.02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000





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Db      36 GlyGlnAlaThrLeuSerGlyIleTyrArgTyrIleMetGlyArgPheAlaPheTyr 55
Qy      466 GCGGCGACTACAGGGCTGGCGCACTCCGTGGCGCAACAACCTTGGCTCAAGACTGC 525
      56 ArgHisAsnArgProGlyTyrGlnAsnSerIleArgHisAsnLeuSerIleAsnGluCys 75
Qy      526 TTGCTCAAGTGTCTGGCGGACCCCTGGCGCCCTGGGCGCAAGACAACCTACTGATCTC 585
      76 PheValIysValProArgAspArgIleAspPro---GlyIysGlySerTyrIlePheLeu 94
Qy      586 AACCCCAACAGCGAGTACACCTTCGCGGAGGCTTCCTCCGCGCGCGCAAGCGCTC 645
      95 AspProAspCysHisAspMetPheGlnHisGlySerPheLeuArgIleArgIlePhe 114
Qy      646 AGCCAC-----CGCGCGCGGTCCCGCG-----CCGCGG 675
      115 ThrArgGlnThrGlyAlaGluGlyThrArgGlyProAlaIleArgIleProLeu 134
Qy      676 CTGGCGCCGAGAGCGCCGCGGCTCCCGCGCG----- 711
      135 ArgAlaThrSerGlnAspProGlyValProAsnAlaThrThrGlyArgGlnCysSerPhe 154
Qy      712 CCGCGCGCGCGCGCG-----GCGCGCGCG 735
      155 ProProGlnLeuProAspProIlyGlyLeuSerPheGlyGlyLeuValGlyAlaMetPro 174
Qy      736 GCGCTG-----CCCGCATGGCTGCGCGCGCGCGCGCAAGAG 774
      175 AlaSerMetCysProAlaThrThrAspGlyArgProArgProMetGluProIlyGln 194
Qy      775 GCGCGCGCGCGCGCGCAAGTTCAGACTCTCGCATGACAGACTCTGCGGAG 834
      195 IleSerThrPro-----Lys 199
Qy      835 CCTCTTCGAGCGCTCGCTCAGAGGAGACGCGCGCGCG-----ACAGCGCTTCACTGGAGC 891
      200 Pro-----AlaCysProGlyGlnLeuProValAlaThrSer 211
Qy      892 GCGCGCGCTTCGCGCGCTGCGCGCGCTTCCCGCG-----CTCCTC 933
      212 SerSerSerCysProAlaPhe---GlyPheProAlaGlyPheSerGlnAlaGluSerPhe 230
Qy      934 CCGCGCGCGCTCAGAGCGCGCTGCTGCGCGCTGCGCGGTACGCGGCGAGCGCGG 993
      231 AsnIysAlaProThrProValIleuSerProGluSerGlyIleGlySerSerTyrGlnCys 250
Qy      994 CGGCTG----- 999
      251 ArgLeuGlnAlaLeuAsnPheCysMetGlyAlaAspProGlyLeuGlnHisLeuLeuAla 270
Qy      1000 GCGCGCGCGAGCGCGAGCTGCCACCGACGCGCGCGCGCTTCGTGTCACCTCTCCG 1059
      271 SerAlaIleProSerProAlaProThrProThrProGlySerIleuArgAlaProLeuPro 290
Qy      1060 GCGCGCGCGCGCGCAAGCACTCGAGCGCGCGCGCGCGCGCGCACTGTATCTGC 1119
      291 -----LeuProThrAspHisIysGluProTyrValAlaGlyGlyPheProValGlnGly 308
Qy      1120 CCGCTGCGGCTGCGCGAGCGCTTCAGCGCGCTTACCGGCTGCTGAGC 1170
      309 GlySerGlyTyrProLeuGlyLeuThrProCysLeuTyrArgThrProGly 325

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; APPLICANT: Tiesenbaum, Heidi
; APPLICANT: Morris, Jason
; APPLICANT: Koweek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351001
; CURRENT APPLICATION NUMBER: US/08/857,076C
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 473
; TYPE: PR
; ORGANISM: Homo sapiens
; US-08-857-076-99

Alignment Scores:
Pred. No.: 5,77e-16 Length: 473
Score: 387.00 Matches: 124
Percent Similarity: 44.36% Conservative: 45
Best Local Similarity: 32.55% Mismatches: 132
Query Match: 17.68% Indels: 80
Gaps: 15

US-10-087-080-31 (1-1209) x US-08-857-076-99 (1-473)

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Qy      130 GGGAGACTCCGCGCGCAAGCGCTCCGCGCGCGCGCGCGCGAGATACGACGAGCGAGC 189
      107 -----AlaLeuSerProSer---GlyMetGlyAlaMetGlyAlaGlnAlaAla 122
Qy      190 GAACAGAGTCGCGAGCGCGCGCGCGCGCGAGAGCGCATCCCGGACGACTGCTGCA 249
      123 SerMetMetAsnGlyLeuGlyProTyrAlaAlaAlaMetAsnProCysMetSerProMet 142
Qy      250 GCGGTGTGCGGAGAGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGG 309
      143 AlaTyrAlaProSerAsnLeuGlyArgSerArgAlaIly-----GlyGlyGlyAsp 159
Qy      310 AGCGGCGAGGTGACGACGACGACGACATATACGCGCGCGCGCGCGCGCGCGCTACTGTAC 369
      160 AlaIysThrPheIysAspSerTyrProHisAla-----LysProProIlySerTyr 176
Qy      370 ATCGCGCTCATTCGCATGCGCATTCGCGGACTCGCGCGCGCGCGCGCTTGAAGCTGAGGAG 429
      177 IleSerIleIleThrMetAlaIleGlnArgAlaProSerIlyMetLeuThrLeuSerGln 196
Qy      430 ATCAAGAGTACCTCATGGGCGAGTCCCTTTTCGCGCGCGCGCGCGCGCGCGCTACG 489
      197 IleTyrIleThrIleMetAspLeuPheProTyrTyrArgGlnAsnGlnAlaGlyProGln 216
Qy      490 AACTCCGTGGCGCAACAACCTTTCGCTCAAGCACTGCTTTCGCAAGTGTCTGCGGACCC 549
      217 AsnSerIleArgHisSerIleuSerPheAsnAspCysPheValIysValAlaArgSerPro 236
Qy      550 TCGCGCGCTCGGGCGAGAGACAACCTACTGATGCTCAACCCCAACAGAGATACACTTC 609
      237 AspIysPro---GlyIysGlySerTyrIlePheIleHisPheProAspSerGlyAsnMetPhe 255
Qy      610 GCGGAGGCGGTCTTCGCGCGCGCGCGAGGCGCTTCAGCGCACCGCGCGCGGTCCCGCG 669
      256 GluAsnGlyCysTyrIleuArgArgGlnIysArg----- 266
Qy      670 CCGCGGCTGCGCGCGCGAGAGAGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCG 729
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Qy      730 GCGCGGCGCTGCGCGCGCGAGCGCTCGCGCGCGCGCG-----CAGAGAGAGCGCGGACG 783
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## RESULT 4

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US-08-857-076-99
; Sequence 99, Application US/08857076C
; Patent No. 6225120
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Koutarou
; APPLICANT: Paterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne

```



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QY 784 CCGCGGCGCAAGTTCCTCAGCTCTTCCATGACAGATCCTCGCGCAAGCCCTTCGCC 843
Db 298 ProSerGly-----AlaSerAsnProSerAlaAspSerProLeuHisArgGlyValHis 315
QY 844 AGCGGTGCGCTCAGGACACAGCGCCCGCGGACGACGCTTACAGTGGGCGCGCGCCCTGC 903
Db 316 -----GlyLysThrGlyGlnLeuGlnGlyAlaProAla 326
QY 904 CCGCGCGTCCCGCGGTTCCTCCCGCGCTCCCGCGCGCGCTCGACAGGCGCTCGCGCG 963
Db 327 ProGlyProAlaAlaSerProGlnThrLeuAsp----- 337
QY 964 CTTCGCGCGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1023
Db 338 -----HisSerGlyAlaThrAlaThrGlyGlyAlaSerGlnLeuLysThrPro 353
QY 1024 -----CCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1062
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QY 1183 TAC 1185
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RESULT 5
US-07-882-292-2
; Sequence 2, Application US/07882292
; Patent No. 5324638
; GENERAL INFORMATION:
; APPLICANT: Tao, Wufan
; APPLICANT: Lai, Eseng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: c/o Cooper and Dunham, 30 Rockefeller
; STREET: Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,292
; FILING DATE: 19920513
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41472
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-07-882-292-2
Alignment Scores:
Score: 1.41e-13
Percent Similarity: 347.00
Best Local Similarity: 40.24%
Query Match: 15.85%
DB: 1
Gaps: 17
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Db 96 ---ProGlnProLeuLeuLeuProProSerAlaAlaLeuAspGlyAlaLysAlaAspAla 114
QY 118 CTGGGCTCAGATGGGAGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177
Db 115 LeuGlyAlaLysGlyLeu-----ProGlyGlyProAlaGlnLeuAlaPro 130
QY 178 CAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
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QY 238 GCAGTGTCTCAGCGCGGTGTGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297
Db 147 -----LysLysGlyAlaGlyLysGlyLysLys 155
QY 298 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 357
Db 156 AspGlyGlnGlyLysGlyLysGlyLys-----AspLysAsnAsnGlyLysThrGlnLysPro 173
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Db 194 ThrLeuAsnGlyLysGlyGlnPheLeuLeuMetLysAsnPheProGlyThrArgGlnLys 213
QY 478 ACGGCTGCGCGCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537
Db 214 GlnGlyTyrGlnAsnSerIleArgHisAsnLeuSerLeuAsnLysCysPheValLysVal 233
QY 538 CTGCGCGACCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 597
Db 234 ProArgHisTyrAspAspPro---GlyLysGlyAlaGlyTyrPheLeuAspProSerSer 252
QY 598 GAGTACACCTTTCGCGCGAGGAGTCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 642
Db 253 AspAspValPheIleGlyLysThrThrGlyLysLeuAlaGlyArgSerThrThrSerArg 272
QY 643 -----CTAGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 690
Db 273 AlaLysLeuAlaPheLysArgAlaArgLeuThrSerThrGlyLeuThrPheMetAsp 292
QY 691 GCGCGCGCGCG-----CTCGCGCGCGCGCGCG-----CGCGCGCGCG 723
Db 293 ArgAlaGlySerLeuTyrTyrPheMetSerProPheLeuSerLeuHisIleProArgAla 312
QY 724 -----CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 753
Db 313 SerSerThrLeuSerTyrAsnGlyThrThrSerAlaGlyTyrProSerHisProMetProGly 332
QY 754 TCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 807
Db 333 SerSerValLeuThrGlnAsnSerLeuGlyAsnAsnHisSerPheSerThrAlaAsnGly 352

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QY 907-----CCGCTC-----CCGCTC 921
Db 393 LeuAmnPro-CysSerValAsnLeuLeuAlaGlyInThrSerTyPhePheProHisVa 412
QY 922 CCGCGCGCTCTCCCGCGGCGCCCTGACAGGCGCTGCTGCGCTGCGCGTACGAGCG 981
Db 412 IProHisProSer-----MethTherScl 420
QY 992 GCGCGCGCGCGCGCTGGCGCGCGCGCGAGCGCCGAGTGCACCGACCGCGCGCCCTC 1043
Db 420 nThrSerThrSerMetSerAlaArgAlaIaSerSerThrSerProGlnAlaProSe 440
QY 1042 CTGCTTGACCTCTCCCGCGGCGCGCC 1069
Db 440 ThrLeuProCysGluSerLeuArgPro 449

RESULT 7
PCT-US93-04102-2
Sequence 2, Application PC/TUS9304102
GENERAL INFORMATION:
APPLICANT: Tao, Wufan
APPLICANT: Lai, Eseng
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04102
FILING DATE: 19930430
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,292
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-04102-2

Alignment Scores:
Pred. No.: 1,416-13 Length: 480
Score: 347.00 Matches: 124
Percent Similarity: 40.24% Conservative: 41
Best Local Similarity: 30.24% Mismatches: 144
Query Match: 15.85% Indels: 101
DB: 5 Gaps: 17

US-10-087-080-31 (1-1209) x PCT-US93-04102-2 (1-480)
QY 22 CCTCGCGCGCGCCACAGGAGCAAGAGGCGCACTGACTCTCGAGAGCGCGCGCGACGAC 81
Db 81 ProProGlnAlaArgGlyAlaProAlaAlaAspAspAspPysGly----- 95

```

OY	82	GGCGCGGTCCCCGCTG-----TCGGGGCGGGAGAGAC-----GACTCC	117
Db	96	---ProGlnProLeuLeuLeuProProSerIaIaLeuAspIyAlaIySaIaAspAla	114
OY	118	CTGGGGCTCAAGATGGGGACTCGCGGCCAAGCCGTCCGCGGGCGCGCCAGATACG	177
Db	115	LeuGlyAlaIySaIyGlu-----ProGlyIyGlyIProAlaIuLeuAlaPro	130
OY	178	CAGGGCGAAGGGAGACAGATGTGGGAGGGCGGGCGGGAGAGAGGATCCGGCA	237
Db	131	ValGlyProAspIyLysGluIySaIySaIyAlaGlyIyGluIu-----	146
OY	238	GCAGGTGCTGCAGCGGTGTGGCGGAGGGCGCGAGCGCGGGCGCGCGCGAGCGCG	297
Db	147	-----LysIySaIyAlaGlyIuGluIyGlyIyS	155
OY	298	GGCGGCGGGGAGCGCGGAGGGGTGACGACAGAAAGCATATACGCGGCGGCCAAGCCC	357
Db	156	AspGlyIuGluIyGlyIyLysGluIy-----AspIySaIySaIyGluIyPro	173
OY	358	CCCTACTGTATCATGCGGTGATCGCCATAGGCATACCGGAGCTCGGCGGGCGGGCTTG	417
Db	174	ProPheMetIyTyraSaIaIaLeuIleuMetuAlaIeIyGlnSerProGluIySaIyGlu	193
OY	418	ACGCTGGCGGAGATCAACAGATACCTCATGGCAAGTTCCCTTTTCCGCGGACAGTAC	477
Db	194	ThiLeuAsnGlyIleTyGluPheIleMetIySaIySaIyProTyTyTyTyArgIuAsnIyS	213
OY	478	ACGGGCTGGCGCAATCCGTGGCGCCAAACCTTGGTCAAGAATGCTTTGTCGAAGTG	537
Db	214	GlnGlyTyPrgIuAsnSerIleArgIhsaIuSerLeuAsnIySeySheValIySaI	233
OY	538	CTGCGCGAAGCCCTCGCGGCGCTGGGGGCAAGACAATATGATGTGTCAACCCCAAGC	597
Db	234	ProArgIhIstTyraAspAspPro---GlyIySaIySaIyTyTyMetIuAspProSerSer	252
OY	598	GAGTACACCTTGCCGCGAGGGGTCTTCCGCGCGCCGCGACAGCC-----	642
Db	253	AspAspValPheIleGlyIyThiThiGlyIyLeuArgIyArgIySerThiThiSerArg	272
OY	643	-----CTCAGCAACGCGGCGCGGCGCCCGCGCGCGGGGTGGGGCCGAGAG	690
Db	273	AlaIySaIeAlaIaPheIySaIyArgIyAlaArgIeIuThiSerThiGlyIeIuThiPheMetAsp	292
OY	691	GCCCCGGGC-----CTCCCCGCGGCCCGG-----CCGCCCCGG	723
Db	293	ArgAlaGlySerLeuTyTyPheMetSerProPheLeuSerLeuIhIshIProArgAla	312
OY	724	-----CCCGCGCCCGCGGCGCTCGGCCCGGATGCGC	753
Db	313	SerSerThiLeuSerTyraSaIyThiThiSerIaIyTyProSerIhIshIProMetProTyTy	332
OY	754	TCGCGCGCGCCGACGAGAGCGGCCAGCCCGCGGCAATCTTCCAGTCC-----	807
Db	333	SerSerValLeuThiGlnAsnSerLeuGlyAsnAsnIhIshIserPheSerThiAlaSaIyGly	352
OY	808	TTCCGCATGACAGCATCTCTCGCGCAG-----CCCTTCGCGAGCGGTCGCTCAAGGAC	861
Db	353	LeuSerValAspArgLeuValAsnGlyIuIleProTyTyAlaThiIhIshIleuThiAla	372
OY	862	ACGGGCGCCCGGAGAGAGCTCAGTGGGGC---GGCGGCGCTGCGCGC-----	906
Db	373	AlaAlaIeAlaIaIaSerValProCysGlyLeuSerValProCysSerIyThiTySer	392
OY	907	-----CCGGTGC-----CCGGCTTC	921
Db	393	LeuAsnPro-CysSerValAsnLeuAlaGlyIuThiTySerTyTyPhePheProIhIsva	412
OY	922	CCCGGCTCCCTCCCGCGGGCGCCCTGCAAGGGCTGCGGCTGCGCGGTACAGCGG	981
Db	412	1ProIhIProSer-----MetIhIserI 420	



```

Best Local Similarity: 63.00%
Query Match: 15.21%
DB: 3
US-10-087-080-31 (1-1209) x US-09-083-351-14 (1-106)

Mismatch: 19
Indels: 2
Gaps: 2

QY 343 CGGCGGGCCC--AGCCCCCTACTGTACATGCGCCTATGCGCATGGCCATCCGCGAC 399
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2  ATgAtgProGluuYsPProProTYserTYLeAlaLeuIlLeValaMeAlaIlleGlnSer 21
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 400 TCGGCGGGCGGCGCTTGAAGCTGGGCGAGATCAAGACATCCATATGCGGCAAGTCCC 455
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 22 SerProThryshArgLeuThryLeuSerGluLeTYrGlnPheLeuGlnSerArgPhePro 41
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 460 TTTTTCGGCGGCGACGACACAGCGGCTGTGGCGCAACTCGTACGCGCACAACTTTCGCTCAAC 519
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 42 PhePheArgIglySerTYrGlnGlyTTPYlsAsnSerValArgHisAsnLeuSerLeuAsn 61
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 520 GACGCTTCTCAAGGCTGCGCGCACCCCTCGCGGCGCCTCGGCGGCAAGACAACTACTCG 579
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 62 GlucySheHeIlleYsLeuProlYsGlyLeuGlyArgPro--GlyYsGlyHisIleTYTTP 80
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 580 ATGCTCAACCCCAACAGCGACGATCAACACTTTCGCCGAGGAGTCTTTCGCCGCGCGCGAC 639
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 81 ThrIleAspProAlaSerGlnPheMetPheGluAsnGlySerPheArgArgArgArgArg 100
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

Alignment Scores: 1.05e-12 Length: 106  
 Pred. No.: 332.00 Matches: 62  
 Score: 79.00% Conservative: 17  
 Percent Similarity: 79.00% Mismatches: 19  
 Best Local Similarity: 62.00% Indels: 2  
 Query Match: 15.17% Gaps: 2  
 DB: 3

US-10-087-080-31 (1-1209) x US-09-083-352-15 (1-106)

QY 343 CGGCGGCCC---AAGCCCCCTACTGTCATCGGCGCTCATGCGCATGCGCATCGCGAC 399  
 |||||  
 Db 2 ATGAGPProGluIyPProProIySerIyRleAlaLeuIleValMetalIeGInsEr 21  
 |||||  
 QY 400 TCGGCGGCGGCGGCTTGAAGCTGCGGAGATCAACAGTACTCTATGGGCAAGTTCCCC 459  
 |||||  
 Db 22 SerProSerIyArGleuThrIeuSerGluIleTyRGlNpheLeuGlnAlaArgPhePro 41  
 |||||  
 QY 460 TTTTTCGCGGCGAGCTACAGCGGCTGCGCACTCCGTGCGCCACCAACCTTTCGCTCAAC 519  
 |||||  
 Db 42 PhePheArGlyAlaTyRGlNglYTrPlyAsnSerValArGhIsnIeuSerLeuAsn 61  
 |||||  
 QY 520 GACTGCTTGTCAAGGTGCTGCGCGACCCCTCGCGGCGGCGCAAGCAACTACTG 579  
 |||||  
 Db 62 GlucyPheIleIyLeuProIySglYleuGlyArgPro---GlyysglYhIstYrTp 80  
 |||||  
 QY 580 ATGCTCAACCCCAACAGGATACACCTTTCGCGGCGGCTTTCGCGGCGGCGCAAG 639  
 |||||  
 Db 81 ThrIeAsPProAlaSerGluPheMetPheGluAsnGlySerPheArGArGArGArG 100  
 |||||

RESULT 12

US-09-083-352-15  
 ; Sequence 15, Application US/09083352  
 ; Patent No. 6207450  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheffield, Val C.  
 ; APPLICANT: Alward, Wallace L.M.  
 ; APPLICANT: Stone, Edwin M.  
 ; APPLICANT: Nishimura, Darryl  
 ; APPLICANT: Pacil, Shiva  
 ; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
 ; TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 ; STREET: One Post Office Square  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109-2170  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/083.352  
 ; FILING DATE: 22-MAY-1998  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Arnold, Beth E.  
 ; REGISTRATION NUMBER: 35,430  
 ; REFERENCE/DOCKET NUMBER: UIA-029.01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-832-1000  
 ; TELEFAX: 617-832-7000  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 106 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-083-352-15

Alignment Scores: 1.05e-12 Length: 106  
 Pred. No.: 332.00 Matches: 62  
 Score: 79.00% Conservative: 17  
 Percent Similarity: 79.00% Mismatches: 19  
 Best Local Similarity: 62.00% Indels: 2  
 Query Match: 15.17% Gaps: 2  
 DB: 3

US-10-087-080-31 (1-1209) x US-09-083-352-15 (1-106)

QY 343 CGGCGGCCC---AAGCCCCCTACTGTCATCGGCGCTCATGCGCATGCGCATCGCGAC 399  
 |||||  
 Db 2 ATGAGPProGluIyPProProIySerIyRleAlaLeuIleValMetalIeGInsEr 21  
 |||||  
 QY 400 TCGGCGGCGGCGGCTTGAAGCTGCGGAGATCAACAGTACTCTATGGGCAAGTTCCCC 459  
 |||||  
 Db 22 SerProSerIyArGleuThrIeuSerGluIleTyRGlNpheLeuGlnAlaArgPhePro 41  
 |||||  
 QY 460 TTTTTCGCGGCGAGCTACAGCGGCTGCGCACTCCGTGCGCCACCAACCTTTCGCTCAAC 519  
 |||||  
 Db 42 PhePheArGlyAlaTyRGlNglYTrPlyAsnSerValArGhIsnIeuSerLeuAsn 61  
 |||||  
 QY 520 GACTGCTTGTCAAGGTGCTGCGCGACCCCTCGCGGCGGCGCAAGCAACTACTG 579  
 |||||  
 Db 62 GlucyPheIleIyLeuProIySglYleuGlyArgPro---GlyysglYhIstYrTp 80  
 |||||  
 QY 580 ATGCTCAACCCCAACAGGATACACCTTTCGCGGCGGCTTTCGCGGCGGCGCAAG 639  
 |||||  
 Db 81 ThrIeAsPProAlaSerGluPheMetPheGluAsnGlySerPheArGArGArGArG 100  
 |||||

RESULT 13

US-09-087-134-14  
 ; Sequence 14, Application US/09087134  
 ; Patent No. 6365711  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Malcolm Whitman and Xin Chen  
 ; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING  
 ; TITLE OF INVENTION: TGF-BETA SUPERFAMILY SIGNALING  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Clark & Elbing LLP  
 ; STREET: 176 Federal Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/087.134  
 ; FILING DATE: 27-MAY-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/047,991  
 ; FILING DATE: 28-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bleker-Brady, Kristina  
 ; REGISTRATION NUMBER: 39,109  
 ; REFERENCE/DOCKET NUMBER: 00246/501002  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-428-0200  
 ; TELEFAX: 617-428-7045  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 544 amino acids  
 ; TYPE: amino acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: other  
 LOCATION: 1...1  
 OTHER INFORMATION: Human FAST-1  
 US-09-087-134-14

Alignment Scores:  
 Pred. No.: 1.68e-12 Length: 544  
 Score: 329.00 Matches: 111  
 Percent Similarity: 37.57% Conservative: 31  
 Best Local Similarity: 29.37% Mismatches: 130  
 Query Match: 15.03% Indels: 107  
 Gaps: 13

US-10-087-080-31 (1-1209) x US-09-087-134-14 (1-544)

QY 325 CGCAGCAGCATATACGCGCGCGCCCGCCCTACTCTGATCATCGCGCTCATCGCC 384  
 DB |||||  
 DB 24 ArgLysArgLysArgLysArgLysArgLysArgLysArgLysArgLysArgLysArgLys 43  
 QY 385 ATGGCGATCCG 444  
 DB |||||  
 DB 44 LeuValIleGlnIleAlaIleProSerArgArgLysLeuIleGlnIleIleArgGlnVal 63  
 QY 445 ATGGCGCAAGTCCCTTTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 504  
 DB |||||  
 DB 64 GlnAlaValPheProIlePheArgLysArgLysArgLysArgLysArgLysArgLysArgLys 83  
 QY 505 AACCTTTCGCTCAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564  
 DB |||||  
 DB 84 AsnLeuSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 103  
 QY 565 AAGGACACTACTGATGCTC 585  
 DB |||||  
 DB 104 LysGlyAsnIlePheIleValAlaValSerLeuIleProAlaGlnIleAlaValArgLeuGln 123  
 QY 586 -----AACCCCAACGCGCGATACACCTTCCGCGCGCGCGCGCGCGCGCGCGCGCG 618  
 DB |||||  
 DB 124 AsnThrAlaLeuGlyArgArgArgArgArgArgArgArgArgArgArgArgArgArgArgArg 143  
 QY 619 GTCTTCCG 651  
 DB |||||  
 DB 143 sPlenGlyProIleValLeuIleGlyArgProTyrArgProIleProIleProIleProIle 163  
 QY 652 CG 669  
 DB |||||  
 DB 163 roSerGlnIlePheSerIleLysSerLeuLeuArgArgSerGlnGlnGlnAlaPro-Trip 182  
 QY 670 CG 696  
 DB |||||  
 DB 183 ProGlnIleAlaLeuAlaProIleAsnSerProValIleProAlaGlnIleThrGlyAsnGlnGlnGln 202  
 QY 697 GGCCTCCCG 756  
 DB |||||  
 DB 203 AlaValProIleProIleProIleProIleProIleProIleProIleProIleProIleProIle 222  
 QY 757 CG 813  
 DB |||||  
 DB 222 uProGlnProIleArgValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 242  
 QY 814 ATGCACAGCATCTCGCAAGCCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 873  
 DB |||||  
 DB 242 oSerProGlnSer-----LeuGlnProGlnLeuSerThrThrAlaGlnIleValSerSerSer 261  
 QY 874 AGCAGCGCTT-----CAGTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 911  
 DB |||||  
 DB 261 yGlyArgSerSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 281  
 QY 912 GCGCGCGTGGCG 965  
 DB |||||

DB 281 uProIleTyrThrProAsnValValMetProLeuAlaProProIleProIleProIleProIle 301  
 QY 966 CTGCGGGTACG 1025  
 DB |||||  
 DB 301 nCysPro-----SerThrSerProAlaTyrTyrGlnVal-----AlaProGln 315  
 QY 1026 GACCG 1080  
 DB |||||  
 DB 315 uThrArgGlnProProGlnIleuLeuGlyAspLeuAlaLeuPheGlnGlnValProIle 335  
 QY 1081 -----CTCGAGCG 1097  
 DB |||||  
 DB 335 oAsnLysSerIleTyrAspValTyrValSerHisProArgAspLeuAlaIleProGlnPro 355  
 QY 1098 CG 1119  
 DB |||||  
 DB 355 oGlyTyrLeuLeuSerTyrCysSerLeu\*\*\*GlySer\*\*\*AspArgGlyArgSerSerLe 375  
 QY 1120 -CCGCTGCGGCTGCG 1164  
 DB |||||  
 DB 375 uProLeuProProProProCys\*\*\*GlnGlyAlaIleAlaArgArg 390

RESULT 14  
 US-09-083-351-12  
 / Sequence 12, Application US/09083351  
 / Patent No. 6087107  
 GENERAL INFORMATION:  
 APPLICANT: Sheffield, Val C.  
 APPLICANT: Alward, Wallace L.M.  
 APPLICANT: Stone, Edwin M.  
 APPLICANT: Nishimura, Daryll  
 APPLICANT: Patil, Shiva  
 TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR  
 TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-2170  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/083,351  
 FILING DATE: 22-MAY-1998  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arnold, Beth E.  
 REGISTRATION NUMBER: 35,430  
 REFERENCE/DOCKET NUMBER: UTA-029.02  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-832-1000  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 106 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-083-351-12  
 Alignment Scores:  
 Pred. No.: 5.09e-12 Length: 106  
 Score: 320.50 Matches: 61  
 Percent Similarity: 71.43% Conservative: 14  
 Best Local Similarity: 58.10% Mismatches: 29

Query Match: 14.64% Indels: 1  
 DB: 3 Gaps: 1  
 US-10-087-080-31 (1-1209) x US-09-083-351-12 (1-106)  
 QY 340 ACGCGGGGGCCCAAGCCCCCTACTGATCATCGCGCTCATGCGCATGCGCATCGCGAC 399  
 |||||  
 Db 2 ThrArgLeuValIysProProIYrSerTYrIleAlaLeuIleThrMetAlaIleLeuGln 21  
 QY 400 TCGCGCGGGGGGCTTGACGCTGCGGAGATCAACGATCACTCATGCGCAAGTTCCCC 459  
 |||||  
 Db 22 SerProIYsIYsArgLeuThrLeuSerGluIleCysGluPheIleSerGlyArgPhePro 41  
 QY 460 TTTTTCGGCGGCGACCTACACGCGGCTGCGGACACTCGGCGCAACAACCTTGCTCAAC 519  
 |||||  
 Db 42 TYrTYrArgGluIYsPheProAlaTrpGlnAsnSerIleArgHisAsnLeuSerLeuAsn 61  
 QY 520 GACTGCTTGCTCAAGGTCTGCGCGACCCCTCGCGGCTTGCGGCGCAAGCAACTACTGG 579  
 |||||  
 Db 62 AspCysPheValIYsIleProArgGluProGlyAsnPro---GlyYsGlyAsnTYrTrp 80  
 QY 580 ATGCTCAACCCCAACAGCGAGTACACTTGCAGCGGGGTCTTCCGCGCGCGCGCAAG 639  
 |||||  
 Db 81 ThrLeuAspProGluSerAlaAspMetPheAspAsnGlySerPheLeuArgArgGly 100  
 QY 640 CGCCTCAGCCACCGC 654  
 |||||  
 Db 101 ArgPheIYsArgGln 105  
 |||||  
 RESULT 15  
 US-09-083-352-12  
 ; Sequence 12, Application US/09083352  
 ; Patent No. 6207450  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheffield, Val C.  
 ; APPLICANT: Alward, Wallace L.M.  
 ; APPLICANT: Stone, Edwin M.  
 ; APPLICANT: Nishimura, Darryl  
 ; APPLICANT: Patel, Shiva  
 ; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
 ; TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: POLEY, HOAG & ELIOT LLP  
 ; STREET: One Post Office Square  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109-2170  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/083,352  
 ; FILING DATE: 22-MAY-1998  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Arnold, Beth E.  
 ; REGISTRATION NUMBER: 35,430  
 ; REFERENCE/DOCKET NUMBER: UIA-029.01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-832-1000  
 ; TELEFAX: 617-832-7000  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 106 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-083-352-12

## Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:
Score:	5,099-12	61	14	1
Percent Similarity:	320.50	61	14	1
Best Local Similarity:	71.43%	61	14	1
Query Match:	58.10%	29	14	1
DB:	14.64%	1	14	1

US-10-087-080-31 (1-1209) x US-09-083-351-12 (1-106)

QY 340 ACGCGGGGGCCCAAGCCCCCTACTGATCATCGCGCTCATGCGCATGCGCATCGCGAC 399  
 |||||  
 Db 2 ThrArgLeuValIysProProIYrSerTYrIleAlaLeuIleThrMetAlaIleLeuGln 21  
 QY 400 TCGCGCGGGGGGCTTGACGCTGCGGAGATCAACGATCACTCATGCGCAAGTTCCCC 459  
 |||||  
 Db 22 SerProIYsIYsArgLeuThrLeuSerGluIleCysGluPheIleSerGlyArgPhePro 41  
 QY 460 TTTTTCGGCGGCGACCTACACGCGGCTGCGGACACTCGGCGCAACAACCTTGCTCAAC 519  
 |||||  
 Db 42 TYrTYrArgGluIYsPheProAlaTrpGlnAsnSerIleArgHisAsnLeuSerLeuAsn 61  
 QY 520 GACTGCTTGCTCAAGGTCTGCGCGACCCCTCGCGGCTTGCGGCGCAAGCAACTACTGG 579  
 |||||  
 Db 62 AspCysPheValIYsIleProArgGluProGlyAsnPro---GlyYsGlyAsnTYrTrp 80  
 QY 580 ATGCTCAACCCCAACAGCGAGTACACTTGCAGCGGGGTCTTCCGCGCGCGCGCAAG 639  
 |||||  
 Db 81 ThrLeuAspProGluSerAlaAspMetPheAspAsnGlySerPheLeuArgArgGly 100  
 QY 640 CGCCTCAGCCACCGC 654  
 |||||  
 Db 101 ArgPheIYsArgGln 105  
 |||||

Search completed: August 27, 2004, 15:36:01  
 Job time : 47.5 sec



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 27, 2004, 15:27:09 ; Search time 165.5 Seconds

(without alignments)  
4596.580 Million cell updates/sec

Title: US-10-087-080-31

Perfect score: 2189  
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Scoring table:

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	Ygapop 10.0	Ygapext 0.5
	Dgapop 6.0	Dgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 1297172 seqs, 31461289 residues

Total number of hits satisfying chosen parameters: 2594344

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-NCPU=6 -ICPU=3 -NO MMAP -LARGEJOURN -NRG SCORES=0 -WAIT -DSPELOCK=100  
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Database: Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	2123	97.0	402	12	US-10-229-345-18	Sequence 18, Appl
2	2123	97.0	402	12	US-10-274-177-18	Sequence 18, Appl
3	2123	97.0	402	15	US-10-087-080-32	Sequence 32, Appl
4	2123	97.0	402	16	US-10-650-112-18	Sequence 18, Appl
5	2081.5	95.1	403	16	US-10-650-112-22	Sequence 22, Appl
6	1597	73.0	400	16	US-10-650-112-23	Sequence 23, Appl
7	1534	70.1	400	16	US-10-650-112-24	Sequence 24, Appl
8	517	23.6	465	14	US-10-205-823-136	Sequence 136, Appl
9	429.5	19.6	553	10	US-09-292-862-2	Sequence 2, Appl
10	415.5	19.0	376	14	US-10-007-280A-221	Sequence 22, Appl
11	388.5	17.7	19662	15	US-10-084-846A-6	Sequence 6, Appl
12	387	17.7	473	9	US-09-844-353A-99	Sequence 99, Appl
13	387	17.7	473	14	US-10-177-293-212	Sequence 212, Appl
14	384.5	17.6	501	9	US-09-963-285-10	Sequence 2, Appl
15	384.5	17.6	501	9	US-09-963-285-7	Sequence 7, Appl
16	384	17.5	494	9	US-09-963-285-7	Sequence 7, Appl
17	372.5	17.0	19723	15	US-10-084-846A-5	Sequence 5, Appl
18	369	16.4	19662	15	US-10-084-846A-6	Sequence 6, Appl
19	366.5	16.7	237	14	US-10-029-386-32327	Sequence 32327, A
20	364	16.6	19652	15	US-10-084-846A-7	Sequence 7, Appl
21	354	16.2	19608	15	US-10-084-846A-8	Sequence 8, Appl
22	351	15.6	19652	15	US-10-084-846A-7	Sequence 7, Appl
23	344	15.7	294	16	US-10-437-963-193697	Sequence 193697, A
24	339.5	15.5	19695	15	US-10-084-846A-3	Sequence 3, Appl
25	338.5	15.5	19725	15	US-10-084-846A-4	Sequence 4, Appl
26	338	15.4	509	16	US-10-471-450-11	Sequence 11, Appl
27	336	15.3	347	9	US-09-844-353A-100	Sequence 100, Appl
28	336	15.0	19608	15	US-10-084-846A-8	Sequence 8, Appl
29	329	15.0	544	13	US-10-044-442-14	Sequence 14, Appl
30	325.5	14.9	625	16	US-10-437-963-165015	Sequence 165015, A
31	323.5	14.4	19723	15	US-10-084-846A-5	Sequence 5, Appl
32	322	14.7	497	16	US-10-437-963-125004	Sequence 125004, A
33	315.5	14.0	19695	15	US-10-084-846A-3	Sequence 3, Appl
34	311.5	14.2	514	16	US-10-437-963-111701	Sequence 111701, A
35	306.5	14.0	417	9	US-09-963-285-4	Sequence 4, Appl
36	305.5	14.0	503	13	US-10-044-442-11	Sequence 11, Appl
37	305	13.9	503	12	US-10-425-114-64093	Sequence 64093, A
38	304.5	13.6	19725	15	US-10-084-846A-4	Sequence 4, Appl
39	303.5	13.9	437	16	US-10-437-963-168762	Sequence 168762, A
40	302.5	13.8	797	14	US-10-156-761-10907	Sequence 10907, A
41	301.5	13.4	595	9	US-09-738-973-187	Sequence 187, Appl
42	301.5	13.4	595	9	US-09-854-133-187	Sequence 187, Appl
43	301.5	13.4	595	14	US-10-144-699A-187	Sequence 187, Appl
44	297.5	13.6	2263	16	US-10-408-765A-2231	Sequence 2231, Appl
45	294	13.4	316	12	US-10-425-114-57324	Sequence 57324, A

## ALIGNMENTS

RESULT 1  
US-10-229-345-18  
; Sequence 18, Application US/10229345  
; Publication No. US20040038220A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKOWITZ, Sanford D.  
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS  
; FILE REFERENCE: CWRU-P01-003  
; CURRENT APPLICATION NUMBER: US/10/229,345  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 402  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-229-345-18

## Alignment Scores:

Pred. No.:	7.07e-93	Length:	402
Score:	2123.00	Matches:	402
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.98%	Indels:	0

DB:	12	Gaps:	0
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Db	21	GluGlyAlaGlyGlySerAspAlaProSerProIleuSerAlaIlaGlyAspAspSerLeu	40
QY	121	GGCTCAGATGGCGGACTGGCGGCGCAAGCCGTCGCGGCGGCGCGCGCCAGAGTATCCAG	180
Db	41	GlySerSerSpGlyAspCysAlaAlaLysProSerAlaGlyGlyGlyAlaAspSerGln	60
QY	181	GGCCACGGCGCAACAGAGTGCAGGAGGCGGCGCGCGCGAGAGAGCGATCCCGCGCA	240
Db	61	GlyAspGlyGlnGlnInsSerAlaGlyGlyGlyProGlyAlaGlnGlnIleIleProAlaIla	80
QY	241	GCTGCTGACAGCGGTGGTGCGGAGGCGCGGAGCGCCGGGCGCGGCGCCACAGCGCGGCG	300
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QY	301	GGCGCGGGGAGCGCGCGGGTGCGACGACGAGCATATACGGGCGGCGCCACAGCCGCC	360
Db	101	GlyAlaGlySerGlyGlnGlyAlaAspSerLysProTyrThrAlaGAPProLysPro	120
QY	361	TACTCGTACATCGCGCTCATCGCATGCGCACATCCGCGCATCTGCGCGGCGGCGCTTGACG	420
Db	121	TyrSerTyrIleAlaIleuIleAlaIleMetAlaIleIleArgSerSerAlaGlyAlaGlyLeuThr	140
QY	421	CTGGCGGAGATCAACGAGTACTTCATATGAGCAAGTTCCCTTTTTCGCGGCGACTACAG	480
Db	141	LeuAlaGlnIleAsnGlnTyrLeuMetGlyLysPheProPheIleArgGlySerTyrThr	160
QY	481	GGCTGGCGCACTCCGTGGCGGCAACAACCTTGCTGCAACGATCTGCTGTAAGTGTCTG	540
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QY	541	CGCGACCCCTCGCGGCGCTGGGGGCAAGGACAATCTAGATGCTCAACCCCAACAGCGAG	600
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D	b		361	LeuarGcylPProAlaAlaGlYglYAlaAhlsHeutyrcysPProleuArgLeuProAlaA	380
O	y		1141	CTGAGAGGGCCTTAGTCCGNCGTCCTTG3GCCGCAACCTGTGTAACCCGGTGAGCGCTC	1200
D	b		381	LeudlnalalaaleValaArgrArgProGlyProhiSleuSerTyPProvalGluhrIeu	400
O	y		1201	CTAGCT 1206	
D	b		401	Leuala 402	
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US-10-274-177-18					
; Sequence 18, Application US/10274177					
; Publication No. US20040038225A1					
; GENERAL INFORMATION:					
; APPLICANT: MARKOWITZ, Sanford D.					
; TITLE OR INVENTION: METHODS FOR CATEGORIZING PATIENTS					
; FILE REFERENCE: CMRU-P01-003					
; CURRENT APPLICATION NUMBER: US/10/274,177					
; CURRENT FILING DATE: 2002-10-18					
; PRIOR APPLICATION NUMBER: US/10/229,345					
; PRIOR FILING DATE: 2002-08-26					
; NUMBER OF SEQ ID NOS: 20					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 18					
; LENGTH: 402					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-274-177-18					
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Pred. No.: 7.07e-93 Length: 402					
Score: 2123.00 Matches: 402					
Percent Similarity: 100.00% Conservative: 0					
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Query Match: 96.98% Indels: 0					
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D	b		21	GUUGlYAlaGlYglYserhsAsphlaProserPProleuserAlaAlaGlYaspsperIeu	40
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O	y		181	GGCGGCGGCGAACAAGATGCGGGAGGCGGGGCCGGGCGGAGAGAAGCGCATCCCGGAGCA	240
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D	b		101	GLYAlaGlYserGlyGluGlyAlaArgrSerItySProyrThArGrProIySProPo	120
O	y		361	TACTGTGATCATGGCGCTCATGCGCATNGGCATCCGGAATCGGCGGGCGGGGCTTGACG	420
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QY 421 CTGGCGGAGATCAACGATGCTCATGGGCAAGTCCCTTTTCCGGCGGACCTACAG 480  
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 QY 481 GGCTGGGCAACTCCGCGGCAACACTTTCGTCACAGACGCTTCGCAAGGCTCG 540  
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 Db 181 ArgAspProSerArgProTyrGlyLysAspAsnTyrTrpMetLeuAsnProAsnSerGlu 200  
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 Db 201 TyrThrPheAlaAspGlyValPheArgArgArgArgLysArgLeuSerHisArgAlaPro 220  
 QY 661 GTCCCGCGCGCGGCGCTGGGGCGGAGAGAGCGCGGCGCTTCGCGCGCGCGCGCGCG 720  
 Db 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240  
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 Db 261 SerProAlaGlyLysPheSerSerSerPheAlaAlaAspSerTrpLeuArgLysProPhe 280  
 QY 841 CGCAGCGCTCGGCTCAGGGAACAAGCGCGCGCGGAGACGCTTCAGTGGGGCGCGCGCG 900  
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 QY 901 TSCCGCGCGCTGCGCGCTTCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 960  
 Db 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320  
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 Db 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360  
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 Db 361 LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380  
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 Db 401 LeuAla 402

# RESULT 3

US-10-087-080-32  
 ; Sequence 32, Application US/10087080  
 ; Publication No. US20030235820A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Markowitz, Sanford David  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; APPLICANT: Case Western Reserve University  
 ; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for  
 ; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer  
 ; FILE REFERENCE: 018501-00084005  
 ; CURRENT APPLICATION NUMBER: US/10/087,080  
 ; PRIOR FILING DATE: 2002-10-25  
 ; PRIOR APPLICATION NUMBER: US 60/272,206  
 ; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: US 60/281,149  
 ; PRIOR FILING DATE: 2001-04-02  
 ; PRIOR APPLICATION NUMBER: US 60/284,555  
 ; PRIOR FILING DATE: 2001-04-17  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 32  
 ; LENGTH: 402  
 ; TYPE: PRN  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: winged helix/forkhead transcription factor (HNF1)  
 ; US-10-087-080-32

## Alignment Scores:

Pred. No.:	7,07e-93	Length:	402
Score:	2123.00	Matches:	402
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.98%	Indels:	0
DB:	15	Gaps:	0

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 Db 1 MetLysLeuGlnValaPheValaProArgAlaAlaHisGlyLysGlnGlnSerPheLeu 20  
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 Db 21 GlnGlyAlaGlyGlySerAspAlaProSerProLeuSerAlaAlaGlyLysPheSerLeu 40  
 QY 121 GGCTCAGATGGAGGACTCG 180  
 Db 41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyValaArgAspThrGln 60  
 QY 181 GCGCAGCGCGCAACAGATGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
 Db 61 GlyAspGlyGlnGlnSerAlaGlyGlyProGlyAlaGlnGlnAlaProAlaAla 80  
 QY 241 GCTGCTGCAAGCGGTGCG 300  
 Db 81 AlaAlaAlaAlaValaValaAlaGlnGlyAlaGlnAlaGlyAlaAlaGlyProGlyAlaGly 100  
 QY 301 GCGCGCGCGGAGGCG 360  
 Db 101 GlyAlaGlySerGlyGlnGlyAlaArgSerLysProTyrThrArgArgProLysProPro 120  
 QY 361 TACTGTCATCGCGCTCATCGCATGGCATCGCGACTCGCGCGCGCGCGCGCGCGCGCG 420  
 Db 121 TyrSerTyrTrpAlaLeuLeuLeuAlaMetAlaAlaGlyAspSerAlaGlyGlyArgLeuThr 140  
 QY 421 CTGGCGGAGATCAACGAGTACTCATGGGCAAGTTCCTTTTCCGCGCGCGCTACAG 480  
 Db 141 LeuAlaGluLeuAsnGluTyrLeuMetGlyLysPheProPhePheArgGlySerTyrThr 160  
 QY 481 GCGTGGCGCACTCGGTGGCGCACAACTTCGCTCAAGATGCTCTCTCAAGGAGCTG 540  
 Db 161 G|TTPArgAsnSerValaArgHisAsnLeuSerLeuAsnSpysPheValLysValLeu 180  
 QY 541 CGGACCCCTCGCGGCGCTGGGGCAAGACAACTACTGATGCTCAACCCCAACAGGAG 600  
 Db 181 ArgAspProSerArgProTyrGlyLysAspAsnTyrTrpMetLeuAsnProAsnSerGlu 200  
 QY 601 TACACCTTGGCCGACGAGGCTTCCTCCGCGCGCGCAAGGCGCTTCAGCCACCGCGCG 660  
 Db 201 TyrThrPheAlaAspGlyValaPheArgArgArgArgLysArgLeuSerHisArgAlaPro 220  
 QY 661 GTCCCGCGCGCGCGCGCTGGGGCGGAGAGAGCGCGGCGCTTCGCGCGCGCGCGCGCG 720  
 Db 221 ValProAlaProGlyLeuArgProGlnGlnAlaProGlyLeuProAlaAlaProProPro 240  
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QY      841  CGAGCGCTGAGCTCGAGGGAACAGCGCCCGGGAACGACGCTTGAAGTGGGCGCGCGCC 900
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Db      301  CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
QY      961  CCGCTCTGCGCGTACGCGCGCGCGAGCGCGCGCTGCGCGCGCGCGCGCGCGAGGTG 1020
Db      321  ProLeuGlyAlaTyrGlyAlaGlyGlnProAlaArgLeuGlyAlaArgGluAlaGluVal 340
QY      1021  CGACCGACGCGCGCGCGCGCTTGTGACCTCTCCCGCGCGCGCGCGCGCGCAAGCCA 1080
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QY      1081  CTCGAGGCGCGCGCGCGCGCGCGCGACGACCTGTACTGCCCTGCGCGCTGCGCGACGC 1140
Db      361  LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380
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Db      401  LeuAla 402

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## RESULT 4

```

US-10-650-112-18
; Sequence 18. Application US/10650112
; Publication No. US20040110712A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CWRU-P01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 402
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-650-112-18

```

## Alignment Scores:

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Pred. No.: 7.07e-93 Length: 402
Score: 2123.00 Matches: 402
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.98% Indels: 0
DB: 16 Gaps: 0

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US-10-087-080-31 (1-1209) x US-10-650-112-18 (1-402)

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QY      1  ATGAAGTTGAGGAGGTTGCTCCCTCGCGCGCGCAAGCGGGAAGAGGAGGAGTGAAGCTG 60
Db      1  MetLysLeuGlnValAlaPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20

```

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QY      61  GAGGCGCGGCGGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db      21  GlnGlyAlaGlyGlySerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
QY      121  GGTCTGAGATGGGAGATGCGCGCGCGCAAGCGCTCCGCGCGCGCGCGCGCGCGCGCGAG 180
Db      41  GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyAlaAlaGlyAspThrGln 60
QY      181  GCGGAGCGGCGAACAAGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db      61  GlyAspGlyGlnGlnSerAlaGlyGlyGlyProGlyAlaGluAlaGlyAlaAlaAla 80
QY      241  GCTGCTGACGCGGTGGTGGCGGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db      81  AlaAlaAlaAlaValAlaValAlaGlnGlyAlaGluAlaGlyAlaAlaGlyProGlyAlaGly 100
QY      301  GCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db      101  GlyAlaGlySerGlyGlnGlyAlaArgSerLysProTyrThrArgArgProLysProPro 120
QY      361  TACTGTGATGATGCGGCTCATGCGCATGCGCATGCGCGACTCGCGCGCGCGCGCGCTGAG 420
Db      121  TyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyAlaGlyLeuThr 140
QY      421  CTGCGGAGATCAACAGTACTCATGCGCAAGTTCCTTTTCCGCGCGCGCGCGCGCGCGCG 480
Db      141  LeuAlaGlnIleAsnGlnIleuMetGlyLysPheProPheArgGlySerTyrThr 160
QY      481  GGTCTGCGCAACTCCGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db      161  GlyTyrArgAsnSerValArgGlnAsnLeuSerLeuAsnAspCysPheValLysValLeu 180
QY      541  CGCGACCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db      181  ArgAspProSerArgProTrpGlyLysAspAsnTyrTrpMetLeuAsnProAsnSerGln 200
QY      601  TACACCTTCGCGCAAGGAGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db      201  TyrThrPheAlaAspGlyValPheArgArgArgArgLysArgLeuSerHisArgAlaPro 220
QY      661  GTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db      221  ValProAlaProGlyLeuAspProGlnGlnAlaProGlyLeuProAlaAlaProProPro 240
QY      721  GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db      241  AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGlnGlnAlaGlyAla 260
QY      781  AGCCCCGCGGGAAGTTCTCCAGCTCTTGCCATGCAGACGATCCTGCGCAAGCCCTTC 840
Db      261  SerProAlaGlyysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
QY      841  CGAGCGCTGAGCTCGAGGGAACAGCGCCCGGGAACGACGCTTGAAGTGGGCGCGCGCC 900
Db      281  ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrpGlyAlaAlaPro 300
QY      901  TGCCCGCGCTGCGCCGCGCTTCCCGCGCTCTCCCGCGCGCGCTGACAGGCGCTGCTG 960
Db      301  CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
QY      961  CCGCTCTGCGCGTACGCGCGCGCGAGCGCGCGCTGCGCGCGCGCGCGCGCGAGGTG 1020
Db      321  ProLeuGlyAlaTyrGlyAlaGlyGlnProAlaArgLeuGlyAlaArgGluAlaGluVal 340
QY      1021  CGACCGACGCGCGCGCGCGCTTGTGACCTCTCCCGCGCGCGCGCGCGCGCGCAAGCCA 1080
Db      341  ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360
QY      1081  CTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db      361  LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380
QY      1141  CTGCGAGCGCGCTTATGTCGACGCTCTGCGCGCGACCTGTGTCGACCGGTGAGAGCGCTC 1200

```

Db 381 LeuGlnAlaIaIeuValArgArgProGlyProHisIeuSerTyrProValGluThrLeu 400  
 QY 1201 CTAGCT 1206  
 Db 401 LeuAla 402

## RESULT 5

US-10-650-112-22  
 ; Sequence 22, Application US/10650112  
 ; Publication No. US20040110712A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MARKOWITZ, Sanford D.  
 ; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS  
 ; FILE REFERENCE: CMRU-P01-044  
 ; CURRENT APPLICATION NUMBER: US/10/650,112  
 ; CURRENT FILING DATE: 2003-08-26  
 ; PRIOR APPLICATION NUMBER: 10/274,177  
 ; PRIOR FILING DATE: 2002-10-18  
 ; PRIOR APPLICATION NUMBER: 10/229,245  
 ; PRIOR FILING DATE: 2002-08-26  
 ; PRIOR APPLICATION NUMBER: 60/406,296  
 ; PRIOR FILING DATE: 2002-08-27  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 22  
 ; LENGTH: 403  
 ; TYPE: PRT  
 ; ORGANISM: HUMAN FOXO1  
 US-10-650-112-22

## Alignment Scores:

Pred. No.: 6,46e-91 Length: 403  
 Score: 2081.50 Matches: 396  
 Percent Similarity: 98.51% Conservative: 1  
 Best Local Similarity: 98.26% Mismatches: 5  
 Query Match: 95.09% Indels: 1  
 Gaps: 1

US-10-087-080-31 (1-1209) x US-10-650-112-22 (1-403)

QY 1 ATGAAGTTGAGGTTTCCTCCGCGCGGCCCAAGGAGCAAGGCGAGTGAACCTG 60  
 Db 1 MetLysIeuGlnValPheValProArgAlaIaHis61YAspLysGlnGlySerAspLeu 20  
 QY 61 GAGGCG 120  
 Db 21 GlnGlyAlaIaGlyIleSerAspAlaProSerProIeuSerAlaIaIaGlyIleSerAspLeu 40  
 QY 121 GGCTCAGATGGGACTGCGCGGCGC---AAGCGCTCCGCGCGCGCGCGCGCGCGCGCG 177  
 Db 41 GlySerAspGlyAspCysAlaIaIaAsnSerProAlaIaIaGlyIleGlyIleAlaArgAspPro 60  
 QY 178 CAGGCG 237  
 Db 61 ProGlyAspGlyGlnGlnIleSerAlaIaGlyIleGlyIleGlnGlnAlaIleProAla 80  
 QY 238 GCAGCTGCTGCACGCGGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297  
 Db 81 AlaAlaIa 100  
 QY 298 GCG 357  
 Db 101 GlyGlyAlaIaGlySerGlyGlnGlyIaArgSerTyrProTyrThrArgArgProLysPro 120  
 QY 358 CCTTACTGTCACATCGCGCTCATCGCATCGCGCATCGCGCATCGCGCGCGCGCGCTTG 417  
 Db 121 ProTyrSerTyrIleAlaIeuIleAlaMetAlaIleArgAspSerAlaIaGlyIaArgLeu 140  
 QY 418 ACGCTGCGGAGATCAACAGAGTACCTCATGGCAAGTCCCTTTTCCGCGCGCGAGCTAC 477  
 Db 141 ThrLeuAlaGlnIleAsnGlnTyrIleuMetGlyLysPheProIlePheArgIleSerTyr 160

QY 478 ACGGCTGGCGCAACTCCGTGCGCCACAACCTTTCGCTCAACGACTGCTTCGCAAGGTG 537  
 Db 161 ThrGlyTyrArgAsnSerValArgHisAsnIleuSerIleuAsnAspCysPheValLysVal 180  
 QY 538 CTGCGCGACCCCTCGCGGCGCTCGGCGCAAGGACACTACTGATGCTCAACCCCAACAC 597  
 Db 181 LeuArgAspProSerArgProTyrGlyLysAspAsnTyrTrpMetIleuAsnProAsnSer 200  
 QY 598 GAGTACACCTTCGCGCGCGGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 657  
 Db 201 GlnTyrThrPheAlaAspGlyValPheArgArgArgArgLysArgLysSerHisArgAla 220  
 QY 658 CCGGTCGCCG 717  
 Db 221 ProValProAlaProGlyIleuArgProGlnGlnAlaProGlyIleuProAlaIaProPro 240  
 QY 718 CCGGCG 777  
 Db 241 ProAlaProAlaIaProAlaSerProArgMetArgSerProAlaArgGlnGlnArg 260  
 QY 778 GCCAGCG 837  
 Db 261 AlaSerProAlaIaGlyLysPheSerSerSerPheAlaIleAspSerIleuArgLysPro 280  
 QY 838 TTCCGCGAGCGCTGCGCTCAGGACAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 897  
 Db 281 PheArgSerArgArgLysArgAspThrAlaProGlyThrThrIleuIleThrGlyAlaIa 300  
 QY 898 CCTTGCCTGCG 957  
 Db 301 ProCysProProIleuProAlaPheProAlaIleuIleProAlaIaIaIaProCysAlaGlyAla 320  
 QY 958 CTGCGCGCTCG 1017  
 Db 321 LeuProIleuCysAlaIaIaGlyIleAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 340  
 QY 1018 GTGCGCACGACG 1077  
 Db 341 ValProProThrAlaProProIleuIleuAlaProIleuProAlaIaIaIaIaIaIaIa 360  
 QY 1078 CCACTCCGAGGCG 1137  
 Db 361 ProIleuArgGlyProAlaIaIaGlyIaIaHisIleuTyrCysProIleuArgIleuProAla 380  
 QY 1138 GCCCTGCGAGCGCGCTTAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1197  
 Db 381 AlaIleuGlnAlaIaIaSerValArgArgProGlyProHisIleuProTyrProValGluThr 400  
 QY 1198 CTCTAGCT 1206  
 Db 401 LeuLeuAla 403

## RESULT 6

US-10-650-112-23  
 ; Sequence 23, Application US/10650112  
 ; Publication No. US20040110712A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MARKOWITZ, Sanford D.  
 ; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS  
 ; FILE REFERENCE: CMRU-P01-044  
 ; CURRENT APPLICATION NUMBER: US/10/650,112  
 ; CURRENT FILING DATE: 2003-08-26  
 ; PRIOR APPLICATION NUMBER: 10/274,177  
 ; PRIOR FILING DATE: 2002-10-18  
 ; PRIOR APPLICATION NUMBER: 10/229,245  
 ; PRIOR FILING DATE: 2002-08-26  
 ; PRIOR APPLICATION NUMBER: 60/406,296  
 ; PRIOR FILING DATE: 2002-08-27  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 23  
 ; LENGTH: 400  
 ; TYPE: PRT

```

: ORGANISM: MOUSE FOXQ1
US-10-650-112-23

Alignment Scores:
Pred. No.: 5.04e-68 Length: 400
Score: 1597.00 Matches: 320
Percent Similarity: 82.27% Conservative: 14
Best Local Similarity: 78.82% Mismatches: 62
Query Match: 72.96% Indels: 10
DB: 16 Gaps: 6

US-10-087-080-31 (1-1209) x US-10-650-112-23 (1-400)
QY 1 ATGAAGTTGAGAGTTCGTCCTCGCGGCGCCAGAGGAGGACAGGAGGACGTCG 60
Db 1 MetLysLeuGluValPheValProArgAlaIahISglYasPluMetGlySerAspLeu 20
QY 61 GAGGCGCGGCGGCGAGCGAGCGCGCCGTCGTCGCGCGGAGAGGAGGACGTCG 120
Db 21 GluGlyAlaGlySerSerAspValProSerProLeuSerAlaIahISglYasPlu 40
QY 121 GGCTCAGATGGGAGCTGCGCGCC---AAGCGTCGCGCGGCGCGGCGCCAGATACG 177
Db 41 GlySerAspGlyAspCysAlaAlaAsnSerProAlaIahISglYasPlu 60
QY 178 CAG---GGCGAGCGGCGAGAGGAGGCGGCGCGGCGCGGCGGCGGCGATCCCG 234
Db 61 GluGlyAlaGlyGlyGlyGluArgAsnSerSerGlyAlaProSerAlaIahISglYasPlu 80
QY 235 GCAGCAGCTGCTGCAGCGGTGTGTGCGAGGCGCGAGGCGCGGCGCGGCGCGGCG 294
Db 81 AlaThrAspAspSerArg-----ThrGlnAlaSerAlaIahISglYasPlu 95
QY 295 GCGGCGCGCGCGGCGGAGCGCGGAGGCGGCGAGGCGGAGGCGGCGGCGGCGG 354
Db 96 AlaGlyAlaGlyAlaGlyGlyGlyGluAlaArgSerSerProGlyThrArgArgProLys 115
QY 355 CCCCCCTACCTGTCATCGGCTCATGCGCCATGCGCATGCGGAGCTCGGCGGCGGCGG 414
Db 116 ProProGlySerGlyLeuAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyArg 135
QY 415 TTGACGCTGGCGGAGATCAACGAGTACCTCATGCGGCAAGTTCCCTTTTTCGCGGAGC 474
Db 136 LeuThrLeuAlaGluIleAsnGluLeuMetGlyLysPheProPheArgGlySer 155
QY 475 TACACGGGCTGCGGCACTCGGTGCGGCAACCTTTCGCTCAGGAGCTGTTGTCAG 534
Db 156 TyrThrGlyTyrPArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLys 175
QY 535 GTGCTGGCGGCGAGCCCTCGCGGCGCTGGGCGGAGGACAACTACTGATGCTCAACCCCAAC 594
Db 176 ValLeuArgAspProSerArgProIleGlyAspAsnGlyTyrIleMetLeuAsnProLys 195
QY 595 AGCAGATACACCTTCGCGGAGGAGTCTTCGCGCGCGCGGCAAGCGGCTCAGGACCGC 654
Db 196 SerGluTyrThrPheAlaAspGlyValPheArgArgArgGlyArgLeuSerHisArg 215
QY 655 GCGCGCGTCCCGCGCGGCGCTCGCGGCGGAGAGGCGCGGCGCTCCCGCC---GCC 711
Db 216 ThrThrValSerAlaSerGlyLeuArgProGluAlaProProGlyProAlaGlyThr 235
QY 712 CCGCGCGCGCGCGCGCGCGCGCTCGCGGCGGAGTACGTCGCGCGCGCGCGGAGAG 771
Db 236 ProGlnProAlaProAlaIahISglYasPluMetGlySerAspLeu 255
QY 772 GAGGCGCGGAGCGCGGCGGAGGTTCTCAGCTCTTCGTCATGACAGCATCTCTCGC 831
Db 256 GluArgSerSerProAlaSerLysPheSerSerSerPheAlaIleAspSerLysLeuSer 275
QY 832 AAGCCCTTCGCGGAGGAGCTGCTCAGAGGAGCAGGCGCGCGGAGAGGAGGAGGAGG 891
Db 276 LysProPheArgSerArgArgAspGlyAspSerAlaLeuGlyValGlnLeuProIleGly 295

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QY 892 GCCGCGCGCTCGCGGCGGCTGTCGCGGCTTCGCCGCGGCGGCGGCGGCGGCGG 951
Db 296 AlaIahProCysProProLeuAlaGlyAlaTyrProAlaLeuLeuProAlaIahISglY 315
QY 952 GCCCTGTCGCGCTTCGCGGCTACGCGGCGGAGCGGCGGCGGCGGCGGCGGCGG 1011
Db 316 AlaLeuLeuProLeuCysAlaTyrGlyAlaSerGluProThrLeuAlaIahISglY 335
QY 1012 GCCGAGGTGCACCGAGCGGCGCGCGCGCTTCGTCGCTCCCGGCGGCGGCGGCG 1071
Db 336 ThrGluValGlnProAlaAla---ProLeuLeuLeuAlaProLeuSerThrAlaAlaPro 354
QY 1072 GCCAAGCCACTCCGAGGCGCG---GCCGCGGCGGCGGCGGAGGAGGAGGAGGAG 1128
Db 355 AlaLysProPheArgGlyProGluThrAlaGlyAlaIahISglYasPluMetGlySerAspLeu 374
QY 1129 CTGCGCGGAGCGCTGCGAGGCGGCGCTTATGTCGCGGCTTCGCGGCGGAGGAGGAG 1188
Db 375 LeuProThrAlaLeuGlnAlaIahISglYasPluMetGlySerThrAlaAlaPro 394
QY 1189 GTGGAGAGCGCTCTAGCT 1206
Db 395 ValGlnThrLeuLeuAla 400

RESULT 7
US-10-650-112-24
: Sequence 24, Application US/10650112
: Publication No. US20040110712A1
: GENERAL INFORMATION:
: APPLICANT: MARKOWITZ, Sanford D.
: TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
: FILE REFERENCE: CWRU-P01-04
: CURRENT APPLICATION NUMBER: US/10/650,112
: CURRENT FILING DATE: 2003-08-26
: PRIOR APPLICATION NUMBER: 10/274,177
: PRIOR FILING DATE: 2002-10-18
: PRIOR APPLICATION NUMBER: 10/229,245
: PRIOR FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: 60/406,296
: PRIOR FILING DATE: 2002-08-27
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 24
: LENGTH: 400
: TYPE: PRT
: ORGANISM: RAT FOX Q1
US-10-650-112-24

Alignment Scores:
Pred. No.: 4.77e-65 Length: 400
Score: 1534.00 Matches: 311
Percent Similarity: 79.90% Conservative: 15
Best Local Similarity: 76.23% Mismatches: 68
Query Match: 70.08% Indels: 14
DB: 16 Gaps: 7

US-10-087-080-31 (1-1209) x US-10-650-112-24 (1-400)
QY 1 ATGAAGTTGAGAGTTCGTCCTCGCGGCGCCAGAGGAGGACAGGAGGACGTCG 60
Db 1 MetLysLeuGluValPheValProArgAlaIahISglYasPluMetGlySerAspLeu 20
QY 61 GAGGCGCGGCGGCGAGCGCGCGCTCCCGGCTGTCGCGGCGGAGAGGAGGACGTCG 120
Db 21 GluGlyAlaGlySerSerAspValProSerProLeuSerAlaIahISglYasPlu 40
QY 121 GGCTCAGATGGGAGCTGCGCGCC---AAGCGTCGCGCGGCGCGGCGCCAGATACG 177
Db 41 GlySerAspGlyAspCysAlaAlaAsnSerProAlaIahISglYasPlu 60
QY 178 CAG---GGCGAGCGGAGAGGAGTGCAGGAGGCGGCGGCGGCGGCGGCGGCGATCCCG 234
Db 61 GluGlyAlaGlyGlyGluArgAsnSerSerGlyAlaSerThrGlnAsp----- 77

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QY 235 GCAGCAGCTGCTCAGAGCGTGTGGCGGAGCGCGC-----GAGCCCGGCGCGCGCG 288
Db 78 -----AspProGluValThrAspGlySerArgThrGlnIleAspProValGly 93
QY 289 CCAGGCGCGGCGCGCGCGCGGAGCGCGGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCG 348
Db 94 ProCysAlaGlySerValGlyGlyGlyGlyGlyAlaArgSerIleProTyrThrArgArg 113
QY 349 CCCAGACCCCTCTACTGATCATCGGCTCATGCGCATGCGCATGCGCATGCGCATGCGCGG 408
Db 114 ProLysProProTyrSerTyrIleAlaIleuIleAlaIleuIleAlaIleuIleAlaIleu 133
QY 409 GGGCGCTTACAGCTGCGGAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCA 468
Db 134 GlyArgLeuThrLeuIleAlaGlnIleAsnGluTyrLeuMetGlyLysPheThrPheArg 153
QY 469 GGCAGGTACAGCGGCGCGCGGAGCTCCGCGCGCGAGCAACCTTTCGTCACAGCTGCTTC 528
Db 154 GlySerTyrThrGlyTyrArgAsnSerValArgGlnAsnLeuSerLeuAsnAspCysPhe 173
QY 529 GTCAAGGTGCTGCGCGAGCCCTCGCGGCGCTGCGGAGAGCAAGCAACTGATGATGCTCA 588
Db 174 ValLysValLeuArgAspProSerArgProTyrGlyLysAspAsnTyrTyrMetLeuAsn 193
QY 589 CCCAACAGCGAGTACACTTTCGCGGAGCGGCTTTCGCGCGCGCGCGCGAGCGCGCTCAGC 648
Db 194 ProAsnSerGluTyrThrPheAlaAspGlyValPheArgArgArgLysArgLeuSer 213
QY 649 CACCGCGCGCGGCTCCCGCGCGCGCGCGCGCGCGCGCGAGAGAGCGCGCGCGCTCCCGCG 708
Db 214 HisArgThrThrValSerAlaSerGlyLeuArgProGluGlnAlaProProGlyProAla 233
QY 709 ---GCCCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGCGCGCATGCGCGCGCGCGCGCG 765
Db 234 GlyThrProGlnProAlaProThrAlaGlySerSerProIleAlaArgSerProAlaArg 253
QY 766 CAGAGGAGCGCGCGAGCGCGCGCGCGCGCAAGTTCTTCAGCTCCTTGCATCGACAGCATC 825
Db 254 GlnGlnGlnGlnGlnSerSerProAlaSerLysPheSerSerSerPheAlaIleAspSerIle 273
QY 826 CTGGCGCAGCGCTTTCGCGAGCGCGCTGCGCTCAGAGGAGCAGCGCGCGCGAGCGCTTAC 885
Db 274 LeuSerLysProPheArgSerArgArgAspGlyAspProAlaLeuGlyValGlnLeuPro 293
QY 886 TGGGCGCGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCTTCGCGCGCGCGCGCG 945
Db 294 TrpSerAlaAlaProCysProProLeuArgAlaTyrProAlaLeuLeuProAlaSerSer 313
QY 946 TGCAGGCGCGCTGCTCCGCTGCGCGGTAACGCGCGCGAGCGCGCGCGCGCTGAGCGCG 1005
Db 314 GlyGlyAlaLeuLeuProLeuCysAlaTyrGlyAlaGlyGluProThrLeuLeuAlaSer 333
QY 1006 CGCGAGCGCGAGGTGCGCAACCGAGCGCGCGCGCGCGCGCGCTTCGCGCTTCCCGCGCGCG 1065
Db 334 ArgGlyAlaGlnValGlnProAlaAla---ProLeuLeuLeuAlaProLeuSerThrAla 352
QY 1066 GCCCGCGCGCAAGCGCATCCCGAGCGCGCG---GCGCGCGCGCGCGCGAGCATGATGCGCGC 1122
Db 353 AlaProAlaLysProPheArgGlyProGlnThrAlaGlyAlaAlaIleuLeuTyrCysPro 372
QY 1123 CTGGGCGCTGCGCGAGCGCTTCGAGCGCGCGCTTACGCGCGCGCTGCGCGCGCATGCTGC 1182
Db 373 LeuArgLeuProThrAlaLeuGlnAlaAlaAlaAlaCysGlyProGlyProHisLeuSer 392
QY 1183 TACCGCGTGGAGAGCGCTCTAGCT 1206
Db 393 TyrArgValGlnThrLeuLeuAla 400

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RESULT 8  
 US-10-205-823-136  
 ; Sequence 136, Application US/10205823  
 ; Publication No. US20030108963A1

```

; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gordatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Woneey, Angela M.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-080-31 (1-1209) x US-10-205-823-136 (1-465)

Alignment Scores:
Pred. No.: 5,266-17 Length: 465
Score: 517.00 Matches: 157
Percent Similarity: 44.21% Conservative: 34
Best Local Similarity: 36.34% Mismatches: 132
Query Match: 23.62% Indels: 109
Gaps: 16

QY 60 GAGGCGCGCGCGCGCGAGCGCGCGCTCCCGCTGTCGCGCGGAGAGCACTCCCT 119
Db 39 GlyGlyGlyGlyGlyProArgLeuAlaValPro----- 49
QY 120 GGGCTCAGATGGAGACTCGCGGCGCGAGCCGCTCGCGGCGCGCGCGCGCGAGATACCA 179
Db 50 -----AlaGlnArgArgArgArgSerTyrAla 60
QY 180 GGGGAGCGCGAGAGAG-----TGCGGG 203
Db 61 GlyLysAspGlnLeuGlnAspLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
QY 204 AGGCGGCGCGCGCGCGAGAGAGCGAGTCGCGCGAGCACTGTCAGCGGTGTCGCGGA 263
Db 81 ProProAlaGlyLysProAlaProProGlyProAlaProAlaAlaGlyAlaGlyAla 100
QY 264 GGGCGGAGGCGGGGCGGGGCGGGGCGAGCGCGCGCGCGCGCGCGCGCGCGAGGCTGC 323
Db 101 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 119
QY 324 ACGCAGAGCATATATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 383
Db 119 AlayAsn---ProLeuVal-----LysProProTyrSerTyrIleAlaLeuIleThr 135
QY 384 CATGCCATCCGCGACCTCGCGCGCGCGCGCGCGCTTACCTGCGGAGATCAAGATACCT 443
Db 135 IMetalAlaIleuGlnSerProLysArgLeuThrLeuSerGlnIleCysGlnPheIle 155

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Db      252 aAlaValProLySerLeuSerProAspSerSerSerSerSerLeuSerSerGlySer 272
QY      865 GCGCCCGGGA-----CGACGCTTCACT-----GGGCGGC 894
Db      272 rProProGlySerLeuProSerAlaArgProLeuSerLeuAspGlyAlaAspSerAlaPr 292
QY      895 GCGCCCTGCGCGCGCGCTGCCCGGCTCCCGCGCTCCCTCC-----935
Db      292 oProPro-ProAla-----ProSerAlaProProProhiShiSerGlnGlyP 308
QY      936 -----CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 966
Db      308 heserValAspAsnIleMetThrSerLeuArgGlySerProGlnSerAlaAlaAlaGln 328
QY      967 TCGCGCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1026
Db      328 eu-----SerSerGlyLeuLeuAlaSerAlaAlaAlaSerS 340
QY      1027 ACCGCGCC-----GCGCTCTCT-----1043
Db      340 eArgAlaGlyIleAlaProProLeuAlaLeuGlyAlaTySerProGlyGlnSerSer 360
QY      1044 -----GCTTGACCTCTCCCGCGCGCGCGCGCGCGCGCGCGCG 1074
Db      360 euTySerSerProCySerGlnThrSerSerAlaGlySerSerGlyGlyGlyGlyG 380
QY      1075 AAGCACTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1128
Db      380 lYAlaGlyAlaAlaGlyGlyAlaGlyAlaGlyThrTyHisCysAsnLeuGlnAla 399
QY      1129 -----CTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1143
Db      400 MetSerLeuTyAlaAlaGlyGlnArgGlyGlyHisLeuGlnGlyAlaProGlyGlyAla 419
QY      1144 CAGGGCGCTTACCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1197
Db      420 GlyGlySerAlaValAspAspProLeuProAspTySerLeuProValThr 437

RESULT 10
US-10-007-280A-221
; Sequence 221, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Hervé
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patent version 3.1
; SEQ ID NO 221
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-221

Alignment Scores:
Pred. No.: 3,39e-12 Length: 376
Score: 415.50 Matches: 128
Percent Similarity: 42.59% Conservative: 33
Best Local Similarity: 33.86% Mismatches: 118
Query Match: 18.98% Indels: 99
Db: 14 Gaps: 15

US-10-087-080-31 (1-1209) x US-10-007-280A-221 (1-376)
QY 232 CCGGAGAGAGCTGCTGCGAGCGGTGTGGCG-----GAGGCGCGC 270

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Db      8 ProGlnAspAlaAlaGlyAlaLeuLeuAlaProGlnThrGlyArgThrValLysGlnPro 27
QY      271 GAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330
Db      28 GlnGlyProProProSerProGlyLysGlyGlyGlyGlyGlyGlyThrAlaProGln 47
QY      331 AAGCCATATACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 390
Db      48 lysProAspProAlaGln--LysProProTySerThrValAlaLeuIleAlaMetAla 66
QY      391 ATCCGCGACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 450
Db      67 lIeArgLysSerAlaGlnLysArgLeuThrLeuSerGlyIleTyGlnIleIleAla 86
QY      451 AAGTTCCCTTTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510
Db      87 lysPheProPheTyGlnLysAsnLysLysGlyTyTrpGlnAsnSerIleArgHisAsnLeu 106
QY      511 TCGCTCAACGACGCTTGTCAGAGTGCTGCGCGCGCGCGCGCGCGCGCG 570
Db      107 SerLeuAsnGlnCysPheIleLysValProArgGlnGlyGlyGln--ArgLysGly 125
QY      571 AACTACTGATGCTCAACCCCAACAGCGAGTACACTTGCGCGCGCGCGCG 630
Db      126 AsnTyTrpThrLeuAspProAlaCysGlnAspMetPheGlnLysLysnTyArgArg 145
QY      631 CCGCGCAAGCGCGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 666
Db      146 ArgArgArgMetLysArgProPheArgProProProAlaHisPheGlnProGlyLysGly 165
QY      667 -----GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 703
Db      166 LeuPheGlyAlaGlyAlaAla--GlyGlyCysGlyAlaAlaGlyAlaGlyAlaAspG 185
QY      704 -----CGCGCGCGCGCG-----715
Db      185 yTyGlyTyLeuAlaProProTyTyLeuGlnSerGlyPheLeuAsnAsnSerTrpPr 205
QY      716 -CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 771
Db      205 OleuProGlnProProSerProMetProTyAlaSerGlyGlnMetAlaAlaAlaAla 225
QY      772 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 826
Db      225 aAlaAlaAlaAlaAlaAlaAlaAlaGlyProGlySerProGlyAlaAlaAlaValVa 245
QY      827 -----TGCGCAAGCGCTTCGCGCGCGCGCGCTCAGGACACAG-----865
Db      245 lLysGlyLeuAlaGlyProAlaAlaSerTyGlyProTyThrArgValGlnSerMetAl 265
QY      866 -----CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 915
Db      265 AleuProProGlyAlaValaAsnSerTyAsnGlyLeuGlyProProAlaAlaProBr 285
QY      916 GCGTTCCCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 975
Db      285 oProProProhiSprohiSpro-----292
QY      976 GCGCGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1035
Db      293 -----HisProhiSAlaHisHis-----298
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QY      1096 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1155
Db      314 -----AlaAlaAlaAlaProProProGlnGlnLeuS 323
QY      1156 GTCCGAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1205

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QY      880 CTTCAgTGGGGCGCGCGCTGCGCGCGCTGCC-----CGCGTTCCCC 924
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Db      261 lAlAla---AlaProAsnGlyLeuProGlyPheSerValGluAsnIleMetThrLeuArgT 280
QY      925 GGGCTGCTGCGCGCGCGCGCTGCGAGGGCCCTGCGCTGCGCGTACGGCGCGGGC 984
      ::: ||||| ||||| |||||
Db      280 hSerProProGlyGlyIleu----- 287
QY      985 GAAGCGCGCGCGCTGGCGCGCGCGAGGCCAGGTGCCACCGCGCGCGCGCTGCTG 1044
      ::: ||||| ||||| ||||| |||||
Db      288 --SerProGlyAlaGlyArgAla-GlyLeuValIvalProProLeuAlaLeuProTyrAla 306
QY      1045 CTTGCACTCTCCCGCGCGCGCGCGCGCGCAAGCCACTCCGAGGCCCGCGCGCGCGCGC 1104
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Db      307 AlAlAlaPro---ProAlAlaIatYrGlyGlnProCysAlaGlnGlyLeuGluAlaGlyAla 325
QY      1105 GCGCACCTGTAC---TGCGCGCGCGCG----- 1128
      ||||| ||||| ||||| |||||
Db      326 AlaGlyGlyTyrGlnCysSerMetArgAlaMetSerLeuTyrThrGlyAlaGluArgPro 345
QY      1129 -----CTGCCCGCGAGCCCTTGCAAGCGCGCGCTTAGTCCGNCGTCT---GGCCCG 1173
      ::: ||||| ||||| ||||| ||||| |||||
Db      346 AlaHisMetCysValProProAlaLeuAspGluAlaLeuSerAspHisProSerGlyPro 365
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Search completed: August 27, 2004, 15:59:01  
Job time : 208.5 secs

OM nucleic - nucleic search, using sw model

Run on: September 2, 2004, 10:29:59 ; Search time 103 Seconds

(without alignments)  
6513.938 Million cell updates/sec

Title:	US-10-087-080-31
Perfect score:	1209
Sequence:	1 atgaagcttgaggtgttcgt.....tggagacgctcctagcttga 1209

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 1365418

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database : Issued\_patents\_NA:\*

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
No.							
1	271.8	22.5	320	4	US-09-833-381-1266		Sequence 1266, App
2	187.6	15.5	1660	5	PCT-US931-644-3		Sequence 3, Appl
3	187.6	15.5	1660	5	PCT-US931-04102-3		Sequence 3, Appl
4	184.4	15.3	1965	4	US-09-420-133-21		Sequence 21, Appl
5	175.6	14.5	3946	3	US-09-083-351-1		Sequence 1, Appl
6	175.6	14.5	3946	3	US-09-083-352-1		Sequence 1, Appl
7	171.6	14.2	1659	3	US-09-083-351-3		Sequence 3, Appl
8	171.6	14.2	1659	3	US-09-083-352-3		Sequence 3, Appl
9	152.8	12.6	2830	3	US-07-083-292-1		Sequence 1, Appl
10	152.8	12.6	2830	2	US-08-331-644-1		Sequence 1, Appl
11	152.8	12.6	2830	5	PCT-US931-04102-1		Sequence 1, Appl
12	134.6	11.1	1309	4	US-09-976-594-927		Sequence 927, App
13	130.2	10.8	1155	2	US-08-331-644-4		Sequence 421, App
14	130.2	10.8	1155	5	PCT-US931-04102-4		Sequence 4, Appl
15	117.6	9.7	5080	4	US-09-976-594-495		Sequence 495, App
16	110.6	9.1	1634	4	US-09-083-134-13		Sequence 13, Appl
17	110.6	9.1	1793	3	US-09-113-309-1		Sequence 1, Appl
18	110.6	9.1	1793	3	US-09-521-109-1		Sequence 1, Appl
19	110.6	9.1	1793	4	US-09-562-337-1		Sequence 1, Appl
20	104.4	8.6	2561	4	US-09-616-289-48		Sequence 48, Appl
21	91.2	7.5	12001	4	US-08-458-568A-11		Sequence 11, Appl
22	88	7.3	2561	4	US-09-616-289-48		Sequence 48, Appl
23	86	7.1	4403765	3	US-09-103-840A-2		Sequence 2, Appl
24	85.4	7.1	152331	3	US-09-103-840A-2		Sequence 16, Appl
25	85	7.0	12425	4	US-09-616-289-50		Sequence 50, Appl
26	84.8	7.0	4411529	3	US-09-103-840A-1		Sequence 1, Appl
27	83.6	6.9	4403765	3	US-09-103-840A-2		Sequence 2, Appl

28	82.8	6.8	1605.4	US-09-087-134-10	Sequence 10, Appl 1
29	82.2	6.8	1200.1	US-08-458-668A-11	Sequence 11, Appl 1
30	81.6	6.7	697.3	US-09-040-084-17	Sequence 17, Appl 1
31	81.6	6.7	697.4	US-09-123-912-17	Sequence 17, Appl 1
32	81.6	6.7	697.4	US-09-643-597-17	Sequence 17, Appl 1
33	81.6	6.7	697.4	US-09-480-084A-17	Sequence 17, Appl 1
34	81.6	6.7	697.4	US-09-542-615A-17	Sequence 17, Appl 1
35	81.6	6.7	697.4	US-09-606-421B-17	Sequence 17, Appl 1
36	81.6	6.7	697.4	US-09-221-107-17	Sequence 17, Appl 1
37	81.2	6.7	4257.2	US-08-590-473-1	Sequence 1, Appl 1
38	81.2	6.7	4257.2	US-09-259-821A-1	Sequence 1, Appl 1
39	81.2	6.7	4257.2	US-08-843-659-1	Sequence 1, Appl 1
40	80.8	6.7	4411589	US-09-103-840A-1	Sequence 1, Appl 1
41	79.6	6.6	1614.4	US-09-616-289-45	Sequence 45, Appl 1
42	78.2	6.5	1578.1	US-08-681-129-1	Sequence 1, Appl 1
43	78	6.5	8438.1	US-07-945-283-1	Sequence 1, Appl 1
44	77.8	6.4	1668.4	US-09-087-134-16	Sequence 16, Appl 1
45	77.2	6.4	1242.8	US-09-616-289-50	Sequence 50, Appl 1

## ALIGNMENTS

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RESULT 1
US-09-833-381-1266
; Sequence 1266: Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833.381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516.448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1266
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(320)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1266

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Query Match	22.5%;	Score 271.8;	DB 4;	Length 320;
Best Local Similarity	94.9%;	Pred. No. 1.3e-35;		
Matches 298;	Conservative	0;	Mismatches 14;	Indels 2;
				Gaps 2

[illegible]

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Db          301 GCCCGCGGACGAC 314

RESULT 2
US-08-331-644-3
; Sequence 3, Application US/08331644
; Patent No. 5976872
;
; GENERAL INFORMATION:
; APPLICANT: Tao, Wufan
; APPLICANT: Lai, Eseng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
;
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,644
; FILING DATE:
;
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,292
; FILING DATE: 13-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41472-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1860 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: CDNA
;
; US-08-331-644-3
;
Query Match          15.5%; Score 187.6; DB 2; Length 1860;
Best Local Similarity 58.3%; Pred. No. 3, 6e-22;
Matches 394; Conservative 0; Mismatches 264; Indels 18; Gaps 3,

QY      8 TGGAGGTGTTCTCCCTCGCGCGGCCCGACAGGAGGACAGTACCTCGAGGGCG 67
Db      421 TCGAGTGTGTGGGGAGGGCGGAGCAGACGAGAGGAGGAGCATGACGAGGGCG 480
QY      68 CGGGCGGCGAGCAGCGCGCGCTCCCGCTGTGCGCGCGGAGACGACTCCCTG3GCTGAG 127
Db      481 GGGCGGGCGCGCGCGCGCGCGCGGTCCCGTTTCCGAGCTCGGCCCGAGCGGCGGAGCGCT 540
QY      128 ATGGGAGACTGCGCGCGCAGACCGCTCCGCGCGCGCGCGCGCGCCACAGAGATACGAGGGCGAGT 187
Db      541 CTTAGCGCCGCGGAGGTGCAATC-----TCGAGGACCTTGAGGAGGAGGAGCAGAG 588
QY      188 GCGACAGAGTCCGGGAGCGCGCGCGCGCGCGAGAGGACGATCCCGCGAGCAGCTGCTG 247
Db      589 ATGACTGTGCTGTGCGCCCCCGCGCTCGCGCTCCCGCGCGCTCCGAGTCTTGCGCCG 648
QY      248 CAGCGGTGTGCGCGAGCGCGCGAGGCGCGGAGCCGCGGCGCGCGCGCGCGCGCGCGCGCG 307
Db      649 CCGCGGCGAGCGGGGTGTGGCGCGGTGTCAGCGCGCGCGCGAGCGGAGGCGCGCGCGAGGTG 708
QY      308 GAGCGCGCGAGGGGTGCAGCGACGACGACATATACGCGCGCGCGCGCAAGCCCCCTCACTCGT 367

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Db      709  GTACGGGCGCGGGGACGGGGGGGGCGCTTAAGAAATCCGCTGCTGAGAGCCGCCCTACTCGT  768
QY      368  ACAATGGGCTCATTCGCCCATGCGCATCTCGCGACTCGCGGGGGCGCTTGAAGCTTGAGCGG  427
Db      769  ACAATGGGCTCATTCACCATGAGCCATCTCTGACAGGCCCAAGAAAGCGCTTGAAGCTCAGCG  828
QY      428  AGATCAACAGAGTACCTCATATGGGCGCAAGTTCCTTTTCCGGGCGAGCTACACGSGGCTGGC  487
Db      829  AGATCTCGAGTTATATAGACGCCGCTTCCCTTACTACCGGAGAAAGTTCCTCCCGCTTGGC  888
QY      488  GCAACTCCGTGCGCCACACCTTTTCGCTCAACGACTCTTGTCAGGTGCTGCGAC  547
Db      889  AGAAGACACATCCGTCACACCTGTGCTCAACGACTGCTTGTCAAGATCCCGGCGCAAC  948
QY      949  ---CGGCAACCCCGGCAAGGGCAACTACTGAGAGCTGACCCGAGTCCGCAATATGT  1005
Db      608  TCGCCAAGCGGAGTTCCTCCGCGCGCGCGCAAGCGCTCAGCCACCGCGCGCGTCCCG  667
QY      1006  TCGACACAGCAGAGTTCTCTGGGCGCGCGCAAGCCTTCA---AGGCGCAGCGCTACTCG  1063
Db      1063  ATCCCGCGCTGGGAC  1078

RESULT 3
PCT-US93-04102-3
; Sequence 3, Application PC/TUS9304102
; GENERAL INFORMATION:
; APPLICANT: Tao, Mufan
; APPLICANT: Lai, Eseng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: John P. White
; STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04102
; FILING DATE: 19930430
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,292
; FILING DATE: 13-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41472A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TELEX: 422523 COOP UI
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1860 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-04102-3

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US-09-083-351-1
; Sequence 1, Application US/09083351
; Patent No. 6087107
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
TITLE OF INVENTION: TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HONG & ELIOT LLP
STREET: One Post Office Square
City: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UTA-029.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 475..2133
US-09-083-351-1

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TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-832-1000  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1659 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-09-083-351-3

Query Match 14.2%; Score 171.6; DB 3; Length 1659;  
 Best Local Similarity 51.3%; Pred. No. 1.3e-19;  
 Matches 483; Conservative 0; Mismatches 444; Indels 15; Gaps 3;

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57 CGGCGGCGAGCAAGCTACTACCGCGGCGCGCGCGCGCGGCGGCGGCGGCGGCG 116
243 TGCTGACGGGTGTGGCGGAGGCGCGGAGGCGCGGCGGCGGCGGCGGCGGCGG 302
117 CATGCGGCGCGCCATGAGCTGTACTGCACTGCGCAGCGCGAGCGAGTACCGGCGG 176
303 CGGCGGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 356
177 CATGCGCGCGCGCTTACGCGCGCTTACAGCGCGGCGGCGGCGGCGGCGGCGGCGG 236
357 CCGCTACTGTACATCGCGCTCATCGCATGCGCATCGCGACTCGCGGCGGCGGCGCTT 416
237 GCCTTAGTACATCGCGCTCATCGCATGCGCATCGAGACGCGCGGCGGCGGCGGCGG 296
417 GAGCGTGGCGGAGTCAACAGATACCTCATGGGCAAGTCCCTTTTTCGCGCGAGCTA 476
297 CACCTGTAAGGAGTATCAACAGATTCATGAGACGCGCTTCCCTTCAACGCGGAGCA 356
477 CAGGCGGTGGCGGCACTCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 536
357 GCGAGGCTTGGGAGAGCATCGCGCATCGCGCATCGCGCATCGCGCATCGCGCATCG 416
417 GCGCGCGAGGAGCAAGAGCC---GGGCAAGGCGAGCTACTGAGCGCTGAGCCGGA 473
597 CAGATACATCTTGGCGGAGGAGTCTTCCCGCGCGCGCGGCGGCGGCGGCGGCGGCG 656
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594 CCGCGAGCGCGCGCGCGCGCGCGCGCGCGAGAGCGGCGGCGGCGGCGGCGGCGGCG 653
771 GAGAGCGGCGGCGCGCGCGCGGCGGAGAGTCTTCAAGCTCTTCCGCGCATGCAACA 830
654 GCGCGCGGTGTGCATCAAGAGCATCAAGAGCGGAGAGCGTATCGTCCCTTGGCGG 713
831 CAGAGCGCTTTCGCGAGCGGTGCGCTCAGGAGACAGGCGCGCGGAGAGAGAGCTT 890
714 GCGCTTGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 773
891 CGCGCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 950
774 GAGCGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 833
951 GCGCGCTGTGCGCGCTTTCGCGGTAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1010
834 GTGCGCGGCGCGCGCTTCAAGCTTGAAGCGGTGAGATTCGCGCGCGCGCGCGCG 893
1011 GCGCGAGGTGTGACCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1070

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Db      894 CCGCGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953
Qy      1071 CCGCAAGCCATCTCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1112
Db      954 GGGGTGCGCGGAGAGCGGCGCGCGGAGCTCAGCTTCGCGCT 995

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RESULT 8  
 US-09-083-352-3  
 Sequence 3, Application US/09083352

Patent No. 6207450  
 GENERAL INFORMATION:  
 APPLICANT: Sheffield, Val C.  
 APPLICANT: Alward, Wallace L.M.  
 APPLICANT: Stone, Edwin M.  
 APPLICANT: Nishimura, Darryl  
 TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
 TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLBY, HOAG & ELIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-2170

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/083,352  
 FILING DATE: 22-MAY-1998

CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arnold, Beth E.  
 REGISTRATION NUMBER: 35,430  
 REFERENCE/DOCKET NUMBER: UIA-029.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-832-1000

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1659 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-09-083-352-3

Query Match 14.2%; Score 171.6; DB 3; Length 1659;  
 Best Local Similarity 51.3%; Pred. No. 1.3e-19;  
 Matches 483; Conservative 0; Mismatches 444; Indels 15; Gaps 3;

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183 CGACGGCGAACAAGTGTGGGAGGCGGCGGCGGAGAGCGATCCCGGAGCAGC 242
57 CGGCGGCGAGCAAGCTACTACCGCGGCGCGCGCGCGCGCGGCGGCGGCGGCGGCG 116
243 TGCTGACGGGTGTGGCGGAGGCGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGG 302
117 CATGCGGCGCGCCATGAGCGTGTACTGCGCACCTTGCAGCGGCGGAGTACCGGCGG 176
303 CGCGGAGGCGGCGGAGGAGTGCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 356
177 CATGCGCGCGCGCTTACAGCGCGCTTACAGCGCGGCGGCGGCGGCGGCGGCGGCG 236
357 CCGCTACTGTACATCGCGCTCATCGCATGCGCATCGCGACTCGCGGCGGCGGCGCTT 416
237 GCCTTAGTACATCGCGCTCATCGCATGCGCATCGAGACGCGCGGCGGCGGCGGCGG 296

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QY	417	GAGCGTGGGGAGANTCAACAGATACCTCATAGGGAAAGTTCCCTTTTTCGGGGACGTA	476
Db	297	CACCTTGAAACGGCATCTACAGATTTCATGAGACCGGCTTCCTCCCTCTACCGGGACAACAA	356
QY	477	CACGGGTGGCGCAACTCCGTGGGCCAACACTTTGGCTCAAGCACTGGCTTGTCAAGT	536
Db	357	GCAGGGGTGGCAAGACATTCGGCCACACCTCTGCTCAAGAGTGTCTGTCAAGAT	416
QY	537	GCTGGCGGACCCCTCGCGGCCCTGGGGGCAAGACAATCTAGTGAATCTCAACCCCAACAG	596
Db	417	GGCGCCGACGACAAAGAGCC---GGGCAAGGCAACTACTGAGCCGTGACCCGCACTC	473
QY	597	CGAGTACACCTTGGCCGACGGGGTCTTTCGGCGCGCGCCGCAAGCGCTCAGCAACCGCGC	656
Db	474	CTACCAACATGTTGAGAAACGAGCTTCTGCGGGCGGGCGCGCTTCAAGAAAGGA	533
QY	657	GCGGTCCCCCGGCGCGGGCTGGGCGCCAGAGAGGCC-----CGGGCTTCCCGCGCG	710
Db	534	CGCGGTGAAGAGACAAAGAGAAAGAAAGACAGGCTGACCTCAAGAGACCGCCCGCGCGG	593
QY	711	CCCGCGCCCGCGCGCCCGCGCCCGGCTCGCCCGGCATAGCGTGGCCCGCGCCGCAAGA	770
Db	594	CCGCAGACCCCGCGCCCGCGCGCCCGGAGAGAGCCCAACGGCAACGGCCCGGTCCGAGCC	653
QY	771	GGAAGGCGGCAAGCCCCCGCGGCAAGTTCTTCAGCTCTTTCGCATTCAGCAGCATCCGCG	830
Db	654	GCGCGCCGTGCACATTCAGAGCATCAAGACCGAAGACGGTACGTGCCCTTCGCGGCCCA	713
QY	831	CAAGCCCTTCCCGCAGCCGCTCGGCTCAAGGACACAGGCCCTCCGGGAGAGAGCTTCAAGTGGG	890
Db	714	GCCCTGTCTCCCGCGCGCCCGCTTGGGCAAGCGGACGCGCGCGGCGGTGCCCAATGCA	773
QY	891	CGCGAGCCCTTACCCCGCGCTGACCGCGTTCGCCCGCGCTCTCCCGCGGGCGCCCTTGACG	950
Db	774	GAGCCCCGACAGCAACAGACAGACGCTGTTCAGACGGGAGACAGCCCCCGGGAGCATTCGC	833
QY	951	GGCCTTGCTGCTCGCTCTGCGGTACGCGCGCGGACAGCGCGCGCGAGTGGGCGCGCGCA	1010
Db	834	GTGCGCGCGGCGGCTCAAGCTTGAGACGTGGGATTCGCGCGCGCGCGCGCGCGCTTC	893
QY	1011	GAGCGAGGTGCAACCGACCGCGCGCGCCCTCTCTGTTGACACTTCTCCGAGCGGGGCC	1070
Db	894	CGCCCGCGCGCGCAACAAAGACAGGGCTTTAGCGGTGACAACATCATGAGCTGCTGG	953
QY	1071	CGCCAGCAACTCCAGAGCCCGGCGGGCGGGCGCGCAACCT	1112
Db	954	GGGGTGCGCGAGACGGCGCGCGCGAGCACTACGCTTCGGGCT	995

## RESULT 9

US-07-882-292-1  
Sequence 1, Application US/07882292  
Parent No. 5324638  
GENERAL INFORMATION:  
APPLICANT: Tao, Wufan  
APPLICANT: Lai, Esseng  
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC ACIDS  
TITLE OF INVENTION: ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: C/o Cooper and Dunham, 30 Rockefeller  
STREET: Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:

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1  APPLICATION NUMBER: US/07/882,292
2  FILING DATE: 19920513
3  CLASSIFICATION: 514
4  ATTORNEY/AGENT INFORMATION:
5  NAME: White, John P
6  REGISTRATION NUMBER: 28,678
7  REFERENCE/DOCKET NUMBER: 41772
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 212-977-9550
10 TELEFAX: 212-664-0525
11 TELEX: 422523 COOP UI
12 INFORMATION FOR SEQ ID NO: 1:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 2830 base pairs
15 TYPE: NUCLEIC ACID
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: cDNA
19 HYPOTHETICAL: N
20 ANTI-SENSE: N
21 FEATURE:
22 NAME/KEY: CDS
23 LOCATION: 443..1882
24 OTHER INFORMATION:
25 FEATURE:
26 NAME/KEY: misc feature
27 LOCATION: 926..1255
28 OTHER INFORMATION: /note= "nucleotide sequence encoding DNA
29 OTHER INFORMATION: binding domain homology"
30 NAME/KEY: misc signal
31 LOCATION: 1883..1895
32 OTHER INFORMATION: /note= "translation termination codon"
33 US-07-882-292-1

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Query Match	12.6%	Score 152.8;	DB 1;	Length 2830;
Best Local Similarity	52.8%	Pred. No. 1.3e-16;		
Matches 409; Conservative	0;	Mismatches 347;	Indels 18;	Gaps 3;

QY	82	GCGCGTTCGCCGTGTGCGCGCGGAGACGACTCCCTGGGCTCATGATGGGAACTGCGCG	141
Db	674	GGCCCCGAGCCCCCGCAGCGCGCGCGGCGCCCTCAGACAGGAGCGAAGAAAGGCCCCCAG	733
QY	142	GCCAAAGCCGTCCGCGGCGCGCGCGCCAGAGATACGAGAGGCGAGCGCGAACAAGTGGC	201
Db	734	CCGGTTTCGTCCCGCGCGTCCGCGCGCCTGAGACGGGCGCAAGGCTGACGCACTTGGAGCC	793
QY	202	GGAAGCGGCGCGGCGCGCGGAGAGCGCATCCCGGACAGCTGTGTGACGCGTGTGGCG	261
Db	794	AAAGCGAAGCGAGCGCGCGCGCGCTTGCGGAGCTGGCGCCGTGGCGCGAGCGAAGAAAGAG	853
QY	262	GAGGCGCGGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGCGT	321
Db	854	AAAGGCGCGCGCGCTGTGGGCGGAGGAGAAAGAGGCGCGCGCGCGCGCAAGAGCGG	913
QY	322	GCAAGCAGCAAGCCATTAAGCGCGCGCC-----AAAGCCCCCTTACTGTAC	369
Db	914	GAGGGGGCAAGAGGCGCGCAAGAAAGAAAGGCAAGTACAGAGAGCGCGCTTACACTAC	973
QY	370	ATCGCGCTATCGCATGCGCATCGCGACTCGCGCGCGCGCGCTTGAACGTGGGAG	429
Db	974	AAAGCGCTCATATGATGGCCATCAAGGAGAGTCCGAGAGAGCGCTGAAGCTTCAACGCG	1033
QY	430	ATCAAGAGTACTCATGGGCAAGTTCCCTTTTCGCGGCACTACAGGAGTGGCGC	489
Db	1034	ATTTAAGAGTTATCATGAAAGACTTCCCTTACTACCGCGAAGCAAGCAGGCTGGCAG	1093
QY	490	AACTCGTGGGCACAACCTTTCGTCTCAAGACTGTGCTCAAGAGTGGTGGCGACCCC	549
Db	1094	AACTCATCCGCAACAACCTGTCCCTCAACMAATGCTTGTGAAGTTACCGGCACATAC	1153
QY	550	TGCGGCGCTGGGGCAAGACAATCTGTGATGCTCAACCCCAACAGCAGATACCTTC	609



NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/04102  
FILING DATE: 19930430  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/862,292  
FILING DATE: 13-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41472A-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2830 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 443..1882  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 926..1255  
OTHER INFORMATION: /note= "nucleotide sequence encoding DNA  
OTHER INFORMATION: binding domain homology"  
FEATURE:  
NAME/KEY: misc signal  
LOCATION: 1883..1885  
OTHER INFORMATION: /note= "translation termination codon"  
PCT-US93-04102-1

Query Match 12.6%; Score 152.8; DB 5; Length 2830;  
Best Local Similarity 52.8%; Pred. No. 1,3e-16;  
Matches 409; Conservative 0; Mismatches 347; Indels 18; Gaps 3;

QY 82 GGGCGCTCCCGCTGTGCGCGCGGAGACGATCCCTGCGCTCAAGTGGGATGCGCG 141  
Db 674 GCGCCGCGAGCCCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 733  
QY 142 GCCAAGCCGTCG 201  
Db 734 CCGCTTCTGCTCCCG 793  
QY 202 GAGAGCG 261  
Db 794 AAGAGCG 853  
QY 262 GAGAGCG 321  
Db 854 AAGAGCG 913  
QY 322 GACAGCGAGCAAGCATATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 369

Db 914 GAGGGGGGAGAGAGGGGCGACAGAGACAGAGCAAGTACAGAGAAAGCCGCTTACCTAC 973  
QY 370 ATGCGCTCATATGCCATATGGCATATCGCGAGCTCGGGCGGGCGCTTGAAGCTGGCGAG 429  
Db 974 AACGCGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033  
QY 430 ATCAAGAGTACCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489  
Db 1034 ATTTAGAGATTTATATGAAAGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1093  
QY 490 AACTCGTGGCG 549  
Db 1094 AACTCATCG 1153  
QY 550 TCG 609  
Db 1154 GACGACCC---GGGCAAGGGGCAACTATCTGATCTGATCTGATCTGATCTGATCT 1210  
QY 610 GCGAGCGGGGTCTTCCG 669  
Db 1211 ATCGAGGACAGACGCGCAAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1270  
QY 670 CCGGCGCTGCG 729  
Db 1271 TTAAAGCG 1327  
QY 730 GCG 789  
Db 1328 TCCCTTCTACTGCG 1387  
QY 790 GGCAGTTCTCCAGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 843  
Db 1388 TTGAGTTACAGGAGCACTCGGCGCTTACCCAGCCAGCCATGCTTACGACG 1441

RESULT 12  
US-09-976-594-927  
Sequence 927, Application US/09976594  
Patent No. 6673549  
GENERAL INFORMATION:  
APPLICANT: Fumess, Michael  
APPLICANT: Buchbinder, Jenny  
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
FILE REFERENCE: PA-0041 US  
CURRENT APPLICATION NUMBER: US/09/976,594  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/240,409  
PRIOR FILING DATE: 2000-10-12  
NUMBER OF SEQ ID NOS: 1143  
SOFTWARE: PERL Program  
SEQ ID NO 927  
LENGTH: 1309  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6673549 3687719CB1  
US-09-976-594-927

Query Match 11.1%; Score 134.6; DB 4; Length 1309;  
Best Local Similarity 57.6%; Pred. No. 1e-13;  
Matches 261; Conservative 0; Mismatches 189; Indels 3; Gaps 1;

QY 340 ACGCGGCG 399  
Db 93 ACTAGCAACCAAGCGCTCCCTTCAAGTACATGCGCGCGCGCGCGCGCGCGCGCGCGCG 152  
QY 400 TCG 459  
Db 153 TCACCGGCG 212  
QY 460 TTTTCCG 519



Db 213 TTCTACCGCAACACCGCCGCTGGCGAAGACAGATCCGCCAATCTGTCTACTCAAC 272  
QY 520 GACTGCTTGTCAAGGTGTGTGCGCAACCCCTGCGGCTTGAGGCAAGCAACTACTG 579  
Db 273 GAGTGTGTTGTCAAGGTGTGCGCGGATGACCGCAAGCC---AGGCAAGGCGAGCTACTG 329  
QY 580 ATGCTCAACCCCAACAGCGAGTACACTTCTGCGGAGGAGTCTTCCGCGCGCGCGCAAG 639  
Db 330 AGCTGAGACCTGACTGCGACGACGATGTTGACAGCGAGCTTCTTACGCGCGCGCG 389  
QY 640 CGCTGACGCGACCGCGCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 699  
Db 390 CGCTTACCGCGAGACAGAGTGTGTGAGGGGACCCGCGCGCGCGCGCGCGCGCGCG 449  
QY 700 CTCCCG 759  
Db 450 CCCCTCAGGGGCG 509  
QY 760 GCCCGCGAGAGGCG 792  
Db 510 TATTCCACAGAGCTGCCAGATCCCAAGGCG 542

RESULT 13  
US-08-331-644-4  
; Sequence 4, Application US/08331644  
; Patent No. 5976872  
; GENERAL INFORMATION:

APPLICANT: Tao, Wufan  
APPLICANT: Lai, Eseng  
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,644  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/882,292  
FILING DATE: 13-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41472-A-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-331-644-4

Query Match 10.8%; Score 130.2; DB 2; Length 1155;  
Best Local Similarity 67.5%; Pred. No. 5,1e-13;  
Matches 199; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 352 AAGCCCCCTTACTCGTACATCGCGCTCATGCGCATGCGCATCTCGGATCTGCGGCGG 411  
Db 499 AAGCGCCCTTACAGCTATATAGCGCTCATCACATGCGCATCAGAACCGCGCAAGAG 558  
QY 412 CGCTGAGCGCTGCGGAGATCAACAGTACCTCATGAGGCAAGTCCCTTTTCCGCGCG 471  
Db 559 AAGATCACTCTAAGCGGACTTACCAATTCATATGAGACCGTTTCCCTTTCTTACCGCG 618  
QY 472 AGCTACAGCGGCTGCGCAACTCCGTCGCGCAACACCTTGTGCTCAACAGACTGCTTGT 531  
Db 619 AACAGAGGCGCTGCGAGAACAGATCCGCGCAACCTGTCACTCAATGAGTGTCTGTG 678  
QY 532 AAGTGTGCGGACCCCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 591  
Db 679 AAGTGTGCGGCGGAGCAAGAGCC---GGGCAAGGAGAGCTTACGAGCGCTGACCGG 735  
QY 592 AACAGGAGTACACCTTGTGCGGACGCGGAGTCTTCCGCGCGCGCGCGCGCGCGCTCA 646  
Db 736 GACTCTACACATGTTGAGAAATGACAGCTTCTGCGCGCGCGCGCGCGCGCTTCA 790

RESULT 14  
PCT-US93-04102-4  
; Sequence 4, Application PC/TUS9304102  
; GENERAL INFORMATION:

APPLICANT: Tao, Wufan  
APPLICANT: Lai, Eseng  
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/04102  
FILING DATE: 19930430  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/882,292  
FILING DATE: 13-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41472A-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US93-04102-4

Query Match 10.8%; Score 130.2; DB 5; Length 1155;  
Best Local Similarity 67.5%; Pred. No. 5,1e-13;  
Matches 199; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 352 AAGCCCCCTTACTCGTACATCGCGCTCATGCGCATGCGCATCTCGGATCTGCGGCGG 411  
Db 499 AAGCGCCCTTACAGCTATATAGCGCTCATCACATGCGCATCAGAACCGCGCAAGAG 558





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Db 961 CCGCTCTGCGCTAGCGGCGGCGGCGAGCCGCGGCTGGGCGCGCGAGGCCAGAGTG 1020

QY 1021 CCACCGACCGGCGCCGCCCTCTCTGCTTGAACCTCTCCGCGCGGCGCCCGCAAAGCCA 1080

Db 1021 CCACCGACCGGCGCCGCCCTCTCTGCTTGAACCTCTCCGCGCGGCGCCCGCAAAGCCA 1080

QY 1081 CTCGAGGCGCGCGCGCGCGCGCGCGAGCCTGTATCTGCCCCCTGCGGCTGCGCGGCG 1140

Db 1081 CTCGAGGCGCGCGCGCGCGCGCGCGAGCCTGTATCTGCCCCCTGCGGCTGCGCGGCG 1140

QY 1141 CTCGAGGCGCGCTTAGTCCGNCSTCTCTGCGCGCGCACTGTCTGATCCCGGTGAGAGCTC 1200

Db 1141 CTCGAGGCGCGCTTAGTCCGNCSTCTCTGCGCGCGCACTGTCTGATCCCGGTGAGAGCTC 1200

QY 1201 CTAGCTTGA 1209

Db 1201 CTAGCTTGA 1209

RESULT 4

US-10-650-112-9

Sequence 9, Application US/10650112

Publication No. US20040110712A1

GENERAL INFORMATION:

APPLICANT: MARKOWITZ, Sanford D.

TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS

FILE REFERENCE: CMRU-P01-044

CURRENT APPLICATION NUMBER: US/10/650,112

CURRENT FILING DATE: 2003-08-26

PRIOR APPLICATION NUMBER: 10/274,177

PRIOR FILING DATE: 2002-10-18

PRIOR APPLICATION NUMBER: 10/229,245

PRIOR FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: 60/406,296

PRIOR FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.2

SEQ ID NO 9

LENGTH: 1209

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (1161)..(1161)

OTHER INFORMATION: n is a,t,g or c

US-10-650-112-9

Query Match 99.9%; Score 1208; DB 17; Length 1209;

Best Local Similarity 100.0%; Pred. No. 9,4e-247;

Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTTGAGGTGCTTCCTCTGCGCGGCGCCACGAGGAGCAAGAGGAGTACCTG 60

Db 1 ATGAAGTTGAGGTGCTTCCTCTGCGCGGCGCCACGAGGAGCAAGAGGAGTACCTG 60

QY 61 GAGGCGCGCGCGCGAGGAGCGGCGCGGCGCGGCGGCTGCTGCGCGGAGAGAGTCTCCCTG 120

Db 61 GAGGCGCGCGCGCGAGGAGCGGCGCGGCGCGGCGGCTGCTGCGCGGAGAGAGTCTCCCTG 120

QY 121 GAGTCAAGTGGGAGCTGCGCGGCGCAAGCCGTCTGCGCGGCGGCGGCGGCGCAAGATACGAG 180

Db 121 GAGTCAAGTGGGAGCTGCGCGGCGCAAGCCGTCTGCGCGGCGGCGGCGGCGCAAGATACGAG 180

QY 181 GCGCAAGCGGCAAGAGTGCAGAGGCGGCGCGGCGCGGCGGCGGAGAGGAGTATCCCGGAGCA 240

Db 181 GCGCAAGCGGCAAGAGTGCAGAGGCGGCGCGGCGCGGCGGCGGAGAGGAGTATCCCGGAGCA 240

QY 241 GCTGTGAGAGGAGTGTGCGGAGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 300

Db 241 GCTGTGAGAGGAGTGTGCGGAGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 300

QY 301 GCGCGGAGGAGCGGCGGAGGAGTGCAGAGCAAGCCATATAGCGGCGGCGGCGGCGGCGGCGGCGG 360

Db 301 GCGCGGAGGAGCGGCGGAGGAGTGCAGAGCAAGCCATATAGCGGCGGCGGCGGCGGCGGCGGCGG 360

Db 301 GCGCGGAGGAGCGGCGGAGGAGTGCAGAGCAAGCCATATAGCGGCGGCGGCGGCGGCGGCGGCGG 360

QY 361 TACTGTATCATGCGGCTATGCGCATGCGCATGCGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420

Db 361 TACTGTATCATGCGGCTATGCGCATGCGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420

QY 421 CTCGAGGAGATCAAGAGTACTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480

Db 421 CTCGAGGAGATCAAGAGTACTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480

QY 481 GCGTGGCGGATCTCCGTGTGCGCGCAAACTTTTGTCTCAAGAGCTGCTGCTCAAGAGGAGGAGG 540

Db 481 GCGTGGCGGATCTCCGTGTGCGCGCAAACTTTTGTCTCAAGAGCTGCTGCTCAAGAGGAGGAGG 540

QY 541 GCGGAGCCCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600

Db 541 GCGGAGCCCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600

QY 601 TACACCTTGGCGGAGCGGAGTCTTTCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660

Db 601 TACACCTTGGCGGAGCGGAGTCTTTCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660

QY 661 GTCCCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720

Db 661 GTCCCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720

QY 721 GCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780

Db 721 GCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780

QY 781 AGCCCGCGGCGGCAAGTCTTCTCACTCTCTTCTGCGGAGGAGTCTTCTGCGGAGGAGGAGGAGGAGG 840

Db 781 AGCCCGCGGCGGCAAGTCTTCTCACTCTCTTCTGCGGAGGAGGAGTCTTCTGCGGAGGAGGAGGAGG 840

QY 841 CGGAGCGG 900

Db 841 CGGAGCGG 900

QY 901 TGCCCGCGG 960

Db 901 TGCCCGCGG 960

QY 961 CCGCTCTGCGGAGTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020

Db 961 CCGCTCTGCGGAGTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020

QY 1021 CCAACCGACGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080

Db 1021 CCAACCGACGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080

QY 1081 CTCGAGGAGCGG 1140

Db 1081 CTCGAGGAGCGG 1140

QY 1141 CTCGAGGAGCGG 1200

Db 1141 CTCGAGGAGCGG 1200

QY 1201 CTAGCTTGA 1209

Db 1201 CTAGCTTGA 1209

RESULT 5

US-10-650-112-25

Sequence 25, Application US/10650112

Publication No. US20040110712A1

GENERAL INFORMATION:

APPLICANT: MARKOWITZ, Sanford D.

TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS

FILE REFERENCE: CMRU-P01-044

CURRENT APPLICATION NUMBER: US/10/650,112

CURRENT FILING DATE: 2003-08-26









QY	715	CCGCGCCGCGCCGCGCCGCCCGCCCTCTGCGCCCGCATGCGCTCGCCCGCCGCGCAGGAGAG	774
Db	709	CAGCCCGCGCCACCGCCGCGCTCCTCCCCCAATCGCGCGCTCGCCCGCTCGCCAGAGAG	768
QY	775	CGCGCGAGCCCGCGGGGAGATTCTTCAGCTCTCTTGCCATTCAGAGCATCTCTGCGCAAG	834
Db	769	GGCTTCACACCCGCGCAGGCAAGTTCTTCAGCTCTCTTGCCATTCAGAGCATCTCTCAGCAAG	828
QY	835	CCCTTCCGCGAGCCCTTGCGCTGAGGGAGACGCGCCCCCGGGAGAGAGCCTTCAGTGGGGCGCC	894
Db	829	CCGTTTCGACACCGCCCGCGAGCGGCGACCCCGGCTCTGGGGGATGCACTACCTTGAGCCCT	888
QY	895	GCGCCCTTGCCCGCGGCTGCCGCGTTCGCCGCGTCTCTCCCGCGCGCCCTGCAAGGAC	954
Db	889	GCTCCCTGCGCGCGCTCGCGCCTATCCCGCGCTCTTCCCGCGCTCGTCCGCGCGTGC	948
QY	955	CTGCTGCGCGCTCTGCGCGTACGCGCGGGGCGAGCCGCGCGCGCTGCGGGGCGCGCGAGGCC	1014
Db	949	CTGCTGCGCGCTCTGTGCTTACGCGCGGGGCGAGCCAGCTGCTGCGCGTGGCGGGGCTC	1008
QY	1015	GAGGTGCCACCGACCGCGCGCGCCCTCTCTGCTTGCACCTCTCCCGCGCGGCGCCGCCCTC	1074
Db	1009	GAGGTG---CAGCCCGCGCGCCCTCCCTGTGCTGCGGCGCCCTCTCCACCGCGGCGCCAGCTC	1065
QY	1075	AAGCGACTCCGAGGCGCGG---CGGCGGGCGGCGCGGACCTGTACTGCGCCCTCGGGGCTG	1131
Db	1066	AAGCATTTCAGAGTCCGGAACCGCGCGCGCGGCGACCTGTACTGCGCCCTTCAGGCTG	1125
QY	1132	CCCGCAGCCCTGCAGCGCGGCTTATGTCGAGCTCTCTGACCCGCACTTGCTACCCGGTGG	1191
Db	1126	CCCGCAGGCTTCGACAGCGGCGCGGCGCTGCGGCTCGGGTCCGGAACCTTCTCAACGGGCTG	1185
QY	1192	GAGAGCGCTCTAGCTTGA	1209
Db	1186	GAGACGCTCTAGCTTGA	1203

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RESULT 8
US-10-152-319A-1814
? Sequence 1814, Application US/10152319A
? Publication No. US20040072160A1
? GENERAL INFORMATION:
? APPLICANT: Mendrick, Donna
? APPLICANT: Porter, Mark
? APPLICANT: Johnson, Kory
? APPLICANT: Higgs, Brandon
? APPLICANT: Castle, Arthur
? APPLICANT: Elashoff, Michael
? TITLE OF INVENTION: Molecular Toxicology Modeling
? FILE REFERENCE: 44921-5089-US
? CURRENT APPLICATION NUMBER: US/10/152,319A
? CURRENT FILING DATE: 2002-05-22
? PRIOR APPLICATION NUMBER: US 60/292,335
? PRIOR FILING DATE: 2001-05-22
? PRIOR APPLICATION NUMBER: US 60/297,523
? PRIOR FILING DATE: 2001-06-13
? PRIOR APPLICATION NUMBER: US 60/298,925
? PRIOR FILING DATE: 2001-06-19
? PRIOR APPLICATION NUMBER: US 60/303,810
? PRIOR FILING DATE: 2001-07-10
? PRIOR APPLICATION NUMBER: US 60/303,807
? PRIOR FILING DATE: 2001-07-10
? PRIOR APPLICATION NUMBER: US 60/303,808
? PRIOR FILING DATE: 2001-07-10
? PRIOR APPLICATION NUMBER: US 60/315,047
? PRIOR FILING DATE: 2001-08-26
? PRIOR APPLICATION NUMBER: US 60/324,928
? PRIOR FILING DATE: 2001-09-27
? PRIOR APPLICATION NUMBER: US 60/330,867
? PRIOR FILING DATE: 2001-11-01
? PRIOR APPLICATION NUMBER: US 60/330,462
? PRIOR FILING DATE: 2001-10-22
? Remaining Prior Application data removed - See File Wrapper or PALM

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```

? NUMBER OF SEQ ID NOS: 2221
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1814
? LENGTH: 1760
? TYPE: DNA
? ORGANISM: Rattus norvegicus
? FEATURE:
? OTHER INFORMATION: Genbank Accession No. NM_022858
US-10-152-319A-1814

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Query Match	59.4%;	Score 717.8;	DB 12;	Length 1760;
Best Local Similarity	78.7%;	Pred. No. 4.6e-143;		
Matches 951; Conservative	0;	Mismatches 233;	Indels 24;	Gaps 7;

QY	8	TGAGAGTGTTCGTCCTTCGCGCGCCACGAGGACAAACAGAGCATGTACCTCGAGGGCG	67
Db	213	TTGGAAGTTCCTGTCCTCCACGCGCAGC-CAGCGGAGCAAAATATGGACGCACTTGGAGGGG	271
QY	68	CGGCGGCGACGACGCGCGCTCCCCGCTGTTCGCGCGCGGAGACGACTCCCTGGGCTCAG	127
Db	272	CCGCGACAGCGAGCGATGCTCATCTCCACTGTTCGCGGCTGTGTGACGACTCTTAAAGCTCAG	331
QY	128	ATGGAGGACTGTGCGCGGCGCAA---GCCTTCGCGGGGCGGCGCGCCAGAGATATCGAGCGCG	184
Db	332	ACGGGAGACTGTGCAAGCCCAACGCCCCGCGCGGGGAGCGGCGCGCGGAGTCTGGAGGTTG	391
QY	185	ACGGCGAACAAGATGCGGAGGCGGAGCGCGGCGCGGAGAGCGATCCCGCAGCAGCTG	244
Db	392	GCGCAGCGAGAGGAATTCGAGTGG-----CGGGCGAGGACCCCAACAGCATC	439
QY	245	CTGACGCGGTGTGTGTGCGGAGGGCGCGGAGGCTCGGGGCGCGGGGCTCAAGCGCGGCGCG	304
Db	440	CCGAGGTGACCGATGTGACGACGAAACGAGGCGCTCCCGGTGTGGGCGCTGTGCGCGGACGCG	499
QY	305	CGGAGGACCGGCGAGGGGTGACGACGACGAGCCATATACCGCGCGCGCCCAAGCGCCCTACT	364
Db	500	TGGCGCGCGGTGTGAGGGCGCGCGGACGAGCCGTACAGCGCGCGGCTCCAGCCCCCTTACT	559
QY	365	CGTACATGCGGCTCATTCGCATGGCCATCCGGACTCGCGGAGCGGCGGCGCTTGAACGCTGG	424
Db	560	CTTACATGCACTCATCGCCATGGCCATTCGCGGACTCGCGGCGGAGACGCTGACGCTGG	619
QY	425	CGGAGTACACGATACCTCATGGGCGAAATCCCTTTTTCGCGGACGCTACACGGGCT	484
Db	620	CCGAGATACAGATTAACCTCATGGGCAAGTTCCTTTTTCGCGGAGGCTACACGGGCT	679
QY	485	GGCGCAACTCGTGTGCGGCCAACCTTTTCGCTCAACGACTGCTGTCAAGGTGCTGGCG	544
Db	680	GGCGCAACTCGTGTGCGGCCAACCTTCGTCAACGACTGTTTGTCAAGGTGCTGGCG	739
QY	545	AACCTTCGCGGCGCTTGGGGCGAAGGACATCTGTGATGCTCAACCCCAACAGCGAGTACA	604
Db	740	AACCTTCGCGGCGCTTGGGGCGAAGGACATTACTGTGATGCTCAACCCCAACAGCGAATACA	799
QY	605	CGTTTCGCGGACGGGGGTCTTCCGCGCGCGCGCAAGCGCTCAGCAACCGCGCGCGGCTCC	664
Db	800	CGTTTCGCGGACGGGGGTCTTCCGCGCGCGCGCAAGCGCTCAGCAACCGCGCAACTCT	859
QY	665	CCGCGGCCCGGCGTGTGCGGCCGAGAGGACCCCGGGCTTCGCCGCCCGCGCGCGCGCGC	724
Db	860	CCGCGATCGGGCTACGGCGGAGAGGACCAACCGGACCTGTGCGGAGACCCCGGACGCCGCGC	919
QY	725	CCGCGCGGCCCGGCGCTCCGCCCGCATGTGCTTCGCCCGCGCGCGCGCAGAGAGCGCGCAGCC	784
Db	920	CCACCGCGGGCTCTTCCCAATGCGCGGCTGCGCGCTTCGCGAGAGAGAGGGCTCCAGCC	979
QY	785	CCGCGGAGCAATTTCTCAGACTCTTTCGCACTGACAGCACTCTTCGAGAGCCTTTCGCA	844
Db	980	CGGAGCAAGATTTCTCAGACTCTTTCGCACTGACAGCACTCTTCAGAGAGCCTTTCGCA	1039
QY	845	GCGGTCCGCTTCAGGAGACAGGCCCGCGGAGCAGCGCTTCACTGATGGGCGCGCGCTTCGCC	904
Db	1040	GCGGCTCCGAGC-GGCACCGGAGCTTGTGGGGGTGACAGTCAACCTGGAGGCTGCTCCCTGCC	1098

QY 905 CGCCGCTGCCCCGCTTCCCGCGCTCTCCCGCGGCGCCCTGAGAGGCTCTGCTGCCGC 964  
Db 1099 CGCGCTGCGCGCTTATCCCGCGCTCTCCCGGCTGTCCGGGAGTGGCCCTGTGCTGCCG 1158  
QY 965 TCTGCGGTACGCGCGCGAGCGAGCGCGGCTGTGGGCGCGCGAGAGCCGAGGCTGCAC 1024  
Db 1159 TCTGTGCTTACGAGCGC-GGCGAGCCACGCTGTGGGCTGTGGGAGCCGAGGTTG---C 1214  
QY 1025 CGACCGCGCGCGCCCTCTCTGTGACCTCTCCCGGCGGCGCCCGCCGCAAGCCACTCC 1084  
Db 1215 AGCCCGCGGCGCGCCCTGTGTGTGGCGCCCTCTCCACCGCGCGCCCGCAAGCCATTTCC 1274  
QY 1085 GAGGCGCGG---CGGCGCGGCGCGCGGCACTGTACTGTGCCCCCTGTGGGCTGTGCCAGAGCC 1141  
Db 1275 GAGGTCGAGAGACCGCGCGCGCGGCGGCACTGTACTGTGCCCCCTGTAGGCTGTCCAGCGGCC 1334  
QY 1142 TGCAGGCGGCGCTTGTGTCGAGCTGTGCGCGCGGCACTGTGTAACCGGTGAGAGCGCTCC 1201  
Db 1335 TGCAGGCGGCGCGCGCGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG 1394  
QY 1202 TAGCTTGA 1209  
Db 1395 TAGCTTGA 1402

## RESULT 9

US-10-027-632-231353/c  
; Sequence 231353, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231353  
; LENGTH: 585  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-231353

Query Match 34.1%; Score 412.6; DB 13; Length 585;  
Best Local Similarity 98.3%; Pred. No. 2.1e-78;  
Matches 415; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 788 CGGCAAGTTCTCCAGCTCTCTTCCGCAATGACAGATCTCTGCGAAGCCCTTCCGCAAGC 847  
Db 585 CGGCAAGTTCTCCAGCTCTCTTCCGCAATGACAGATCTCTGCGAAGCCCTTCCGCAAGC 526  
QY 848 GTGCGCTGAGGAGACAGCGCGCGCGGAGAGAGCTTCACTGAGGAGCGCGCGCTGCGCGC 907  
Db 525 GCGCGCTGAGGAGACAGCGCGCGCGGAGAGAGCTTCACTGAGGAGCGCGCGCTGCGCGC 466  
QY 908 CGTGCCTGAGGAGACAGCGCGCGCGGAGAGAGCTTCACTGAGGAGCGCGCGCTGCGCGC 967

Db 465 CGCTGCCCGGCTTCCCGCGGCTCTCCCGGAGGCGCCCTGAGAGGCTCTGCTGCCCTCT 406  
QY 968 GCGGCTTACGCGCGGAGCGAGCGCGGCTGTGGGCGCGCGGAGCCGAGGCTGACCGA 1027  
Db 405 GCGGCTTACGCGCGGAGCGAGCGCGGCTGTGGGCGCGCGGAGCCGAGGCTGACCGA 346  
QY 1028 CGCGGCGCGCGCTCTGCTGCACTCTCCCGGCGGCGCGCGCGCGCGCAAGCACTCCGAG 1087  
Db 345 CGCGGCGCGCGCTCTGCTGCACTCTCCCGGCGGCGCGCGCGCGCGCAAGCACTCCGAG 286  
QY 1088 GCGCGGCGCGCGGCGCGGCGGCACTGTACTGTGCCCCCTGTGGGCTGTGCCAGG 1147  
Db 285 GCGCGGCGCGCGGCGCGGCGGCACTGTACTGTGCCCCCTGTGGGCTGTGCCAGG 226  
QY 1148 GCGGCTTACGCGCGGAGCGCGGCGGAGCGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG 1207  
Db 225 GCGGCTTACGCGCGGAGCGCGGCGGAGCGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG 166  
QY 1208 GA 1209  
Db 165 GA 164

## RESULT 10

US-10-027-632-231353/c  
; Sequence 231353, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231353  
; LENGTH: 585  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-231353

Query Match 34.1%; Score 412.6; DB 16; Length 585;  
Best Local Similarity 98.3%; Pred. No. 2.1e-78;  
Matches 415; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 788 CGGCAAGTTCTCCAGCTCTCTTCCGCAATGACAGATCTCTGCGAAGCCCTTCCGCAAGC 847  
Db 585 CGGCAAGTTCTCCAGCTCTCTTCCGCAATGACAGATCTCTGCGAAGCCCTTCCGCAAGC 526  
QY 848 GTGCGCTGAGGAGACAGCGCGCGCGGAGAGAGCTTCACTGAGGAGCGCGCGCTGCGCGC 907  
Db 525 GCGCGCTGAGGAGACAGCGCGCGCGGAGAGAGCTTCACTGAGGAGCGCGCGCTGCGCGC 466  
QY 908 CGTGCCTGAGGAGACAGCGCGCGCGGAGAGAGCTTCACTGAGGAGCGCGCGCTGCGCGC 967  
Db 465 GCGTGCCTGAGGAGACAGCGCGCGCGGAGAGAGCTTCACTGAGGAGCGCGCGCTGCGCGC 406  
QY 968 GCGGCTTACGCGCGGAGCGCGGAGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG 1027



QY 681 GCCCGAGAGAGCCCGGAGCTTCCCGCGCCCGCCCGCGCCCGCGCCCGCTC 740  
Db 1111 CCCCCAGTCTCTGCTGCTGCGCGCGAGCCGAGAGAGAGCGCGAGCCCGGAC 1170  
QY 741 GCGCCCGAGTGGCGTGGCGCGCGCGCGAGAGAGAGCGCGAGCCCGCGAGTTC 800  
Db 1171 CCGCGCGCGCTTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1224  
QY 801 CAGCTCTTGGCCATGAGAGCATCTGCGCAAGCCCTTCCGAGCGCTGCGCTCA 860  
Db 1225 CCGCGCGCTAGCGCTGCGCTGAGAGCTGCGCGCTTACGCGCGCGCGCTC 1284  
QY 861 CAGCGCGCGCGAGAGCGCTTCAAGTGGAGCGCGCGCGCGCGCGCGCGCGCT 920  
Db 1285 CTTCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1344  
QY 921 CCGCGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 980  
Db 1345 GCGCGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1404  
QY 981 GCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCGAGTGCACCGAGCG 1040  
Db 1405 GCAACCGCGCT--CGCGCGCGCGCTTACCGCGCGCGCGCGCGCGCGCG 1462  
QY 1041 CCGCTTGGACCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1100  
Db 1463 GCGCGCGCGCGCTTCAAGCGCTGCGCGCTGCGCTTCTTCATGAGAGCAT 1522  
QY 1101 CCGCGCGAGCATCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1160  
Db 1523 AGCTTGGCG 1582  
QY 1161 NCCTCTGCGCGCGAGCTGCG 1182  
Db 1583 TCGCGCTGCGCTGCGCGGTGG 1604

RESULT 13  
US-10-172-118-1045  
; Sequence 1045, Application US/10172118  
; Publication No. US20030224374A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Chris  
; APPLICANT: Van de Vijver, Laura  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-175-999  
; CURRENT FILING DATE: 2002-06-14  
; PRIORITY FILING DATE: 2002-05-14  
; PRIORITY FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 1045  
; LENGTH: 2487  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: NM\_004472  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-1045

Query Match 16.7%; Score 201.4; DB 13; Length 2487;  
Best Local Similarity 52.1%; Fred. No. 8.1e-34;  
Matches 574; Conservative 0; Mismatches 512; Indels 16; Gaps 5;

QY 83 CCGCGTCCCGCGCTGCGCGCGAGAGCATCCCTGGGCTCAGATGGGAGCTGCGCG 142

Db 517 CGACGAGAGAGGCGCGGTGGCGCGGCCCGCGCTGGCTGTCCCGCGAGCGCGCGCG 576  
QY 143 CC--AAGCGTCCCGCGCGCGCGCGCGAGAGATTCAGAGGCGAGCGCGAGAGAGTSC 200  
Db 577 GCGCGCTGTGACGCGCGCGAGAGAGAGTGTGAGAGTCTGGAGAGAGAGAGAGAGCA 636  
QY 201 GAGAGGCGCGCGCGCGCGAGAGAGAGATTCGCGAGAGAGTGTGAGAGAGTGTG 260  
Db 637 TGAACATCTGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 696  
QY 261 GAGAGGCGCGAGAGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGAGG 320  
Db 697 GCGCGGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 753  
QY 321 TGCAGCGAGAGAGAGATATAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 380  
Db 754 CCGCGGTAGCGCGCGCGAGAGAGCGCGGTGAGAGCGCGCGCGCGCGCGCGCG 813  
QY 381 CCGCATAGCGCATTCGCGAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 440  
Db 814 CACTAGGCGCATTCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 873  
QY 441 CCGTATGGAGAGTTCCTCTTTTTCGCGCGAGCTGAGAGGCTGCGCGAGCTCG 500  
Db 874 CATAGCG 933  
QY 501 CCAAGACCTTTCGCTCAAGAGCTTTCGTAAGAGTGTGCGAGCGCGCGCGCGCG 560  
Db 934 CCAAGACCTTTCGCTCAAGAGCTTTCGTAAGAGTGTGCGAGCGCGCGCGCGCG 990  
QY 561 GCGCGAGAGAGAGAGTGTGTAAGAGTGTGTAAGAGTGTGTAAGAGTGTGTA 620  
Db 991 GCGCGAGAGAGAGTGTGTAAGAGTGTGTAAGAGTGTGTAAGAGTGTGTA 1050  
QY 621 CTTCG 680  
Db 1051 CTTCGCGCGCGAGAGAGGCGCTTCAAGCGCGCGCGCGCGCGCGCGCGCG 1110  
QY 681 GCGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 740  
Db 1111 CCGCGAGTCTGTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1170  
QY 741 GCGCGCGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 800  
Db 1171 CCGCGCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1224  
QY 801 CAGCTCTTGGCATGAGAGCATCTTGGCGAGAGCGCGCGCGCGCGCGCGCG 860  
Db 1225 CCGCGCGCTTACGCGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1284  
QY 861 CAGCGCGCGCGAGAGCGCTTCAAGTGGAGCGCGCGCGCGCGCGCGCGCG 920  
Db 1285 CTTCGCGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1344  
QY 921 CCGCGCGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 980  
Db 1345 GCGCGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1404  
QY 981 GCGCGAGCG 1040  
Db 1405 GCAACCGCGCT--CGCGCGCGCGCTTACCGCGCGCGCGCGCGCGCGCG 1462  
QY 1041 CCGCTTGGACCTTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1100  
Db 1463 GCGCGCGCGCGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1522  
QY 1101 CCGCGCGAGCATCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1160  
Db 1523 AGCTTGGCG 1582  
QY 1161 NCCTCTGCGCGCGAGCTGCG 1182  
Db 1583 TCGCGCTGCGCTGCGCGGTGG 1604

RESULT 14  
US-10-205-823-135  
Sequence 135, Application US/10205823  
Publication No. US20030108963A1  
GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Endege, Wilson O.  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Gorbacheva, Bella  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Kametkar, Shubhangi  
APPLICANT: Monsey, Angela M.  
APPLICANT: Zhao, Karen  
APPLICANT: Ghatt, Karen  
APPLICANT: Anderson, Dustin  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF PROSTATE CANCER  
FILE REFERENCE: MRI-044  
CURRENT APPLICATION NUMBER: US/10/205,823  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307,982  
PRIOR FILING DATE: 2001-07-25  
PRIOR APPLICATION NUMBER: 60/314,356  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/325,020  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 60/341,746  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/362,158  
PRIOR FILING DATE: 2002-03-05  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 135  
LENGTH: 2487  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-205-823-135

Query Match 16.7%; Score 201.4; DB 15; Length 2487;  
Best Local Similarity 52.1%; Pred. No. 8.1e-34;  
Matches 574; Conservative 0; Mismatches 512; Indels 16; Gaps 5;

QY 83 CGCCGCTCCCGCTGTGCGCGCGGAGAGACATCCCTGGGCTCAGATGGGAGCTGGCGG 142  
DB 517 CGACGACGAGGCGCGCGCGGCGCGGCGCGGCGCTGCTGCTCCCGCGCAGCGCGCGGCGG 576  
QY 143 CC--AAGCCGTCGCGCGCGCGCGCGCGCAGAGATACGACGAGCGAGCGGCAACAGATGC 200  
DB 577 GCGGCGCTGTACGCGCGGAGAGACGAGCTGAGAGATCTGAGAGAGAGAGAGAGAGAG 636  
QY 201 GGGAGCGCGCGCGCGCGCGCGGAGGAGGAGATCCCGGAGAGCTGTGACGCGGTGGGCGC 260  
DB 637 TGACATCTGTGCGCGCGCGCGCTGTGCGGCGCTCCCGCGCGCGCGCGCGCGCGCGCGC 696  
QY 261 GAGGCG 320  
DB 697 GCGCGCGCGAGAGAGCGCGGTGGGCGCGG---CGCGCGCGCGCGCGCGCGCGCGCGCGG 753  
QY 321 TGCACGACGCAAGCCATATAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 380  
DB 754 CGCGGCTAGCGCGCGCGCAAGAACCGCTGTGTAGAGCGCGCGCGCGCGCGCGCGCGCT 813  
QY 381 CGCATGCGCATCCCGCATCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 440  
DB 814 CACTATGCGCATCTGCGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 873  
QY 441 CCTCATGCGCAAGTTCCCTTTTTCGCGCGCGAGCTACACGCGCGCGCGCGCGCGCGCGCG 500  
DB 874 CATGAGCGCGCGCGCTTCCCTACTACCGGAGAGAGTTCCCGCGCGCGCGCGCGCGCGCG 933

QY 501 CCACAACTTTCGCTCAACAGATGCTGTCAAGGTGTGGAGACCCCTCGCGCCCTG 560  
DB 934 CCAACACTTTCGCTCAACAGATGCTGTCAAGGTGTGGAGACCCCTCGCGCCCTG 990  
QY 561 GGGCAAGAGCACTACTGATGTCAACCCCAAGAGAGTACCTTCGCGCGAGGGT 620  
DB 991 GGGCAAGAGCACTACTGATGTCAACCCCAAGAGAGTACCTTCGCGCGAGGGT 1050  
QY 621 CTTCCG 680  
DB 1051 CTTCCG 1110  
QY 681 GCGCGAGAGAGCG 740  
DB 1111 CGCGAGCTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1170  
QY 741 GCGCGAGAGAGCG 800  
DB 1171 CG 1224  
QY 801 CAGCTCTTTCGCTATGACAGATCTGTGCGCAAGCTTTCGCGAGCGCTTCAGGGA 860  
DB 1225 CG 1284  
QY 861 CAGCG 920  
DB 1285 CTTCCG 1344  
QY 921 CCG 980  
DB 1345 GCG 1404  
QY 981 GCGCGAGCG 1040  
DB 1405 GCACCGCGCT--CG 1462  
QY 1041 CCTGCTGACCTCTCCCG 1100  
DB 1463 GCG 1522  
QY 1101 CGCGCGCGCACTGTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1160  
DB 1523 AGCTTGGCG 1582  
QY 1161 NGCTCTGCGCGCGCACTGTGTG 1182  
DB 1583 TCGCGCTGCGCGCGCGCGGTGG 1604

RESULT 15  
US-09-968-007A-802  
Sequence 802, Application US/09968007A  
Publication No. US20040115625A1  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign  
FILE REFERENCE: 689290-71  
CURRENT APPLICATION NUMBER: US/09/968,007A  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US/60/237,172  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,173  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,278  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,294  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,295  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,316  
PRIOR FILING DATE: 2000-10-02



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 2, 2004, 16:45:04 ; Search time 96 Seconds

(without alignments)  
2323.857 Million cell updates/sec

Title: US-10-087-080-32

Perfect score: 402

Sequence: 1 MKLEFVPPRAHSDKQGS...ALVRRGPHLSYVETLLA 402

Scoring table:

Oligo  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 segs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1360453

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+pn.model -DEV=x.lh  
-Q/cg2\_1/USPTO.spool/US10087080/runat.27082004.104128.13731/app.query.fasta.1.583  
-DB=Issued Patents NA -QEXT=firststep -SUFFIX=Oligo.rni -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -INITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10087080@CGN 1.1.56@runat.27082004.104128.13731 -NCP=6 -ICU=3  
-NO MMAP -LARGEOUTERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA:  
1: /cg2\_6/prodata/2/ina/5A.COMB.seq:\*  
2: /cg2\_6/prodata/2/ina/5B.COMB.seq:\*  
3: /cg2\_6/prodata/2/ina/6A.COMB.seq:\*  
4: /cg2\_6/prodata/2/ina/6B.COMB.seq:\*  
5: /cg2\_6/prodata/2/ina/PCTUS.COMB.seq:\*  
6: /cg2\_6/prodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	32	8.0	4	US-09-833-381-1266	Sequence 1266, App
2	14	3.5	4	US-09-833-381-1266	Sequence 927, App
3	12	3.0	4	US-08-331-644-3	Sequence 3, Appl
4	12	3.0	4	US-08-331-644-3	Sequence 3, Appl
5	10	2.5	4	US-09-252-991A-710	Sequence 710, App
6	10	2.5	4	US-08-331-644-4	Sequence 4, Appl
7	10	2.5	4	US-08-331-644-4	Sequence 4, Appl
8	10	2.5	4	US-09-252-991A-623	Sequence 623, App
9	10	2.5	4	US-09-616-289-45	Sequence 45, App
10	10	2.5	4	US-09-083-351-3	Sequence 3, Appl
11	10	2.5	4	US-09-083-351-3	Sequence 3, Appl
12	10	2.5	4	US-09-220-132-21	Sequence 21, Appl

13	10	2.5	4	US-09-616-289-48	Sequence 48, Appl
14	10	2.5	3	US-09-083-351-1	Sequence 1, Appl
15	10	2.5	3	US-09-083-352-1	Sequence 1, Appl
16	10	2.5	4	US-09-858-664A-1	Sequence 1, Appl
17	10	2.5	4	US-10-274-978-1	Sequence 1, Appl
18	10	2.5	4	US-10-274-978-1	Sequence 1, Appl
19	10	2.5	4	US-08-348-006B-6	Sequence 6, Appl
20	10	2.5	4	US-08-800-825A-6	Sequence 6, Appl
21	10	2.5	4	US-09-158-657-6	Sequence 6, Appl
22	10	2.5	4	PCT-US94-10166-6	Sequence 6, Appl
23	10	2.5	4	US-09-023-655-879	Sequence 879, App
24	10	2.5	4	US-09-616-289-50	Sequence 50, Appl
25	10	2.5	4	US-09-335-409-1	Sequence 1, Appl
26	10	2.5	4	US-09-568-102-1	Sequence 1, Appl
27	10	2.5	4	US-09-567-969-1	Sequence 1, Appl
28	10	2.5	4	US-09-568-480-1	Sequence 1, Appl
29	10	2.5	4	US-09-568-486-1	Sequence 1, Appl
30	10	2.5	4	US-09-568-472-1	Sequence 1, Appl
31	10	2.5	4	US-09-567-899-1	Sequence 1, Appl
32	10	2.5	4	US-09-443-501A-2	Sequence 2, Appl
33	10	2.2	4	US-09-404-879A-304	Sequence 304, App
34	10	2.2	4	US-09-338-933-304	Sequence 304, App
35	10	2.2	4	US-09-215-681-304	Sequence 304, App
36	10	2.2	4	US-09-216-003A-304	Sequence 304, App
37	10	2.2	4	US-09-056-556-165	Sequence 165, App
38	10	2.2	4	US-09-072-967-165	Sequence 165, App
39	10	2.2	4	US-09-072-967-165	Sequence 165, App
40	10	2.2	4	US-09-072-967-165	Sequence 165, App
41	10	2.2	4	US-09-072-967-165	Sequence 165, App
42	10	2.2	4	US-09-325-932A-93	Sequence 251, App
43	10	2.2	4	US-09-056-556-179	Sequence 179, App
44	10	2.2	4	US-09-072-967-179	Sequence 179, App
45	10	2.2	4	US-09-072-967-179	Sequence 179, App

#### ALIGNMENTS

RESULT 1  
US-09-833-381-1266  
Sequence 1266, Application US/09833381  
Patent No. 6672186  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs  
FILE REFERENCE: 5800-119  
CURRENT APPLICATION NUMBER: US/09/833,381  
CURRENT FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: 09/516,448  
PRIOR FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 2050  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1266  
LENGTH: 320  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(320)  
OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-1266

#### Alignment Scores:

Pred. No.: 8.56e-19  
Score: 32.00  
Percent Similarity: 97.83%  
Best Local Similarity: 97.83%  
Query Match: 7.96%  
DB: 4  
Gaps: 0

US-10-087-080-32 (1-402) x US-09-833-381-1266 (1-320)

Qy 220 ProValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProPro 239



DB 92 CCGGTCCCGCGCGGCTGCGCGCCGAGAGAGCCCGCGGCTCCCGCGCGCCGCGCN 151  
QY 240 Pro-Ala-Pro-Ala-Pro-Ala-Ser-Pro-Arg-Met-Lys-Ser-Pro-Ala-Arg-Gln-Glu-Lys 259  
DB 152 CCGCGCGCGCGCGCGCGCGCGCTGCGCGCGCATGCGCTCGCGCGCCGCGCGAGAGAGCG 211  
QY 259 GAlaSerProAlaGly 264  
DB 212 CGCAGCGCGCGCGG 227

RESULT 2  
US-09-976-594-927  
Sequence 927, Application US/09976594  
Patent No. 6673549  
GENERAL INFORMATION:  
APPLICANT: Furness, Michael  
APPLICANT: Buchbinder, Jenny  
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
FILE REFERENCE: PA-0041 US  
CURRENT APPLICATION NUMBER: US/09/976,594  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/240,409  
PRIOR FILING DATE: 2000-10-12  
NUMBER OF SEQ ID NOS: 1143  
SOFTWARE: PERL Program  
SEQ ID NO 927  
LENGTH: 1309  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6673549 3687719CB1  
US-09-976-594-927

Alignment Scores:  
Pred. No.: 0.00731 Length: 1309  
Score: 14.00 Matches: 14  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.48% Indels: 0  
Gaps: 0  
DB: 4

US-10-087-080-32 (1-402) x US-09-976-594-927 (1-1309)

QY 118 Lys-Pro-Phe-Tyr-Ser-Tyr-Ile-Ala-Ileu-Ile-Ala-Met-Lys 131  
DB 105 AAGCTCCCTACAGCTACATCGCCCTTATGCTATGGCATC 146

RESULT 3  
US-08-331-644-3  
Sequence 3, Application US/08331644  
Patent No. 5976872  
GENERAL INFORMATION:  
APPLICANT: Tao, Wufan  
APPLICANT: Lai, Eseng  
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,644  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/882,292  
FILING DATE: 13-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41472-A-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1860 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-331-644-3

Alignment Scores:  
Pred. No.: 0.516 Length: 1860  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.99% Indels: 0  
Gaps: 0  
DB: 2

US-10-087-080-32 (1-402) x US-08-331-644-3 (1-1860)

QY 167 ArgHisAsnLeuSerLeuAsnAspCysPheValIys 178  
DB 900 CGTCACACCTGTGCTCAACGACTGCTTGCTCAAG 935

RESULT 4  
PCT-US93-04102-3  
Sequence 3, Application PC/TUS9304102  
GENERAL INFORMATION:  
APPLICANT: Tao, Wufan  
APPLICANT: Lai, Eseng  
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/04102  
FILING DATE: 19930430  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/882,292  
FILING DATE: 13-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41472A-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1860 base pairs



TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US93-04102-3

Alignment Scores:  
Pred. No.: 0.516 Length: 1860  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.99% Indels: 0  
Gaps: 0

US-10-087-080-32 (1-402) x PCT-US93-04102-3 (1-1860)

Qy 167 ArgHisAsnIeuSerLeuAsnAspCysPheValIys 178  
Db 900 CGTCACACCTGTGCTGCTCAGCAGCTGCTGTCAG 935

RESULT 5  
US-09-252-991A-710/c  
Sequence 710, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 710  
LENGTH: 780  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-710

Alignment Scores:  
Pred. No.: 11.7 Length: 780  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.49% Indels: 0  
Gaps: 0

US-10-087-080-32 (1-402) x US-09-252-991A-710 (1-780)

Qy 240 ProAlaProAlaAlaProAlaSerProArg 249  
Db 190 COTGCACGAGCGGCTCCAGCTTCTCCGCGT 161

RESULT 6  
US-08-331-644-4  
Sequence 4, Application US/08331644  
Patent No. 5976872  
GENERAL INFORMATION:  
APPLICANT: Tao, Wufan  
APPLICANT: Lai, Eseng  
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,644  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/882,292  
FILING DATE: 13-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41472-A-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-331-644-4

Alignment Scores:  
Pred. No.: 16.9 Length: 1155  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.49% Indels: 0  
Gaps: 0

US-10-087-080-32 (1-402) x US-08-331-644-4 (1-1155)

Qy 118 LysProProTyrSerTyrIleAlaIleu 127  
Db 499 AAGCCGCTACAGCTATATAGCGCTCATC 528

RESULT 7  
PCT-US93-04102-4  
Sequence 4, Application PC/TUS9304102  
GENERAL INFORMATION:  
APPLICANT: Tao, Wufan  
APPLICANT: Lai, Eseng  
TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: c/o Cooper and Dunham, 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/04102  
FILING DATE: 19930430  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/882,292  
FILING DATE: 13-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41472A-PCR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCR-US93-04102-4

Alignment Scores:  
Pred. No.: 16.9 Length: 1155  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.49% Indels: 0  
DB: 5 Gaps: 0

US-10-087-080-32 (1-402) x PCR-US93-04102-4 (1-1155)

QY 118 lvsProProTyrSerTyrIleAlaLeuIle 127  
DB 499 AMGGCGCCCTACAGCTAATAGCGCTCATC 528

RESULT 8  
US-09-252-991A-623  
Sequence 623, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252.991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074.788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094.190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 623  
LENGTH: 1488  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-623

Alignment Scores:  
Pred. No.: 21.3 Length: 1488  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.49% Indels: 0  
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-252-991A-623 (1-1488)

QY 240 ProAlaProAlaProAlaSerProArg 249  
DB 1329 CCGCACCGCGCGCTCCAGCTTCGCCGCT 1358

RESULT 9  
US-09-616-289-45  
Sequence 45, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616.289  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517.849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979.608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031.930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048.547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 45  
LENGTH: 1614  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1614)  
US-09-616-289-45

Alignment Scores:  
Pred. No.: 23 Length: 1614  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.49% Indels: 0  
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-616-289-45 (1-1614)

QY 236 AlaAlaProProAlaProAlaPro 245  
DB 532 GCCGCGCGCGCGCGCGCGCGCGCGCGCTCC 561

RESULT 10  
US-09-083-351-3  
Sequence 3, Application US/09083351  
Patent No. 6087107  
GENERAL INFORMATION:  
APPLICANT: Sheffield, Val C.  
APPLICANT: Stone, Edwin M.  
APPLICANT: Nishimura, Darryl  
APPLICANT: Patil, Shiva  
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR  
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN  
TITLE OF INVENTION: TRANSCRIPTION FACTOR  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/083.351  
FILING DATE: 22-MAY-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-029.02

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1659 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-083-351-3

Alignment Scores:  
Pred. No.: 23.6  
Score: 10.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.49%  
DB: 3  
Gaps: 0

US-10-087-080-32 (1-402) x US-09-083-351-3 (1-1659)

QY 118 LysProProTySerTyrIleAlaLeuIle 127  
Db 232 AAGCGCCCTATAGCTACATCGGCTCATC 261

RESULT 11  
US-09-083-352-3  
Sequence 3, Application US/09083352  
Patent No. 6207450  
GENERAL INFORMATION:  
APPLICANT: Sheffield, Val C.  
APPLICANT: Alward, Wallace L.M.  
APPLICANT: Stone, Edwin M.  
APPLICANT: Nishimura, Darryl  
APPLICANT: Patil, Shiva  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/083,352  
FILING DATE: 22-MAY-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-029.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1659 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-083-352-3

Alignment Scores:  
Pred. No.: 23.6  
Length: 1659

Score: 10.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.49%  
DB: 3  
Gaps: 0

US-10-087-080-32 (1-402) x US-09-083-352-3 (1-1659)

QY 118 LysProProTySerTyrIleAlaLeuIle 127  
Db 232 AAGCGCCCTATAGCTACATCGGCTCATC 261

RESULT 12  
US-09-220-132-21  
Sequence 21, Application US/09220132  
Patent No. 6506607  
GENERAL INFORMATION:  
APPLICANT: Shyjan, Andrew W.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT  
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 07334-074001  
CURRENT APPLICATION NUMBER: US/09/220,132  
CURRENT FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 60/079,303  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: US 60/068,821  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 191  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 21  
LENGTH: 1965  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-220-132-21

Alignment Scores:  
Pred. No.: 27.6  
Score: 10.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.49%  
DB: 4  
Gaps: 0

US-10-087-080-32 (1-402) x US-09-220-132-21 (1-1965)

QY 118 LysProProTySerTyrIleAlaLeuIle 127  
Db 190 AAGCGCCCTACTCTGACATCGGCTCATC 219

RESULT 13  
US-09-616-289-48  
Sequence 48, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53

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SOFTWARE: FastSPQ for Windows Version 4.0
? SEQ ID NO. 48
? LENGTH: 2561
? TYPE: DNA
? ORGANISM: Oryctolagus cuniculus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (246) ... (1895)
US-09-616-289-48

Alignment Scores:
Pred. No.:          35.4           Length:      2561
Score:              10.00          Matches:       10
Percent Similarity: 100.0%         Conservative: 0
Best Local Similarity: 100.0%      Mismatches:   0
Query Match:        2.49%          Indels:       0
DB:                  4             Gaps:         0

US-10-087-080-32 (1-402) x US-09-616-289-48 (1-2561)

Oy      236 AlaAlaProProAlaProAlaProAlaPro 245
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RESULT 14
US-09-083-351-1
Sequence 1, Application US/09083351
Patent No. 6087107
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Pacil, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
NUMBER OF INVENTION: TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-029.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 475..2133
US-09-083-351-1

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Alignment Scores:			
Pred. No.:	52.9	Length:	3946
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-09-083-352-1			
Sequence 1, Application US/09083352			
Patent No. 6207450			
GENERAL INFORMATION:			
APPLICANT: Sheffield, Val C.			
APPLICANT: Alward, Wallace L.W.			
APPLICANT: Stone, Edwin M.			
APPLICANT: Nishimura, Darryl			
APPLICANT: Pacil, Shiva			
TITLE OF INVENTION: GLIACOVA THERAPEUTICS AND DIAGNOSTICS			
TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR			
NUMBER OF SEQUENCES: 22			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: FOLEY, HOAG & ELIOT LLP			
STREET: One Post Office Square			
CITY: Boston			
STATE: MA			
COUNTRY: USA			
ZIP: 02109-2170			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent in Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/083,352			
FILING DATE: 22-MAY-1998			
CLASSIFICATION: 514			
ATTORNEY/AGENT INFORMATION:			
NAME: Arnold, Beth E.			
REGISTRATION NUMBER: 35,430			
REFERENCE/DOCKET NUMBER: UIA-029.01			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 617-832-1000			
TELEFAX: 617-832-7000			
INFORMATION FOR SEQ ID NO: 1:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 3946 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: cDNA			
FEATURE:			
NAME/KEY: CDS			
LOCATION: 475..2133			
US-09-083-352-1			
Alignment Scores:			
Pred. No.:	52.9	Length:	3946
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.49%	Indels:	0
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US-10-087-080-32 (1-402) x US-09-083-352-1 (1-3946)			
Qy	118 LysProProTySerTyTlleAlaLeuIle 127		
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Job time : 101 secs

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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 2, 2004, 18:04:14 ; Search time 598 seconds

(without alignments)  
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Title: US-10-087-080-32

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Searched: 3267054 seqs, 2485319735 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6525383

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1  
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-FAPOP=6 -FAPEXT=7 -YAPOP=60 -YAPEXT=60 -DELOP=6 -DELEXT=7

## Database :

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
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- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	402	100.0	1209	13	US-10-229-345-9	Sequence 9, Appl
2	402	100.0	1209	16	US-10-274-177-9	Sequence 31, Appl
3	402	100.0	1209	17	US-10-087-080-31	Sequence 9, Appl
4	402	100.0	1209	17	US-10-650-112-9	Sequence 25, Appl
5	324	80.6	1212	17	US-10-650-112-25	Sequence 26, Appl
6	114	28.4	1203	17	US-10-650-112-27	Sequence 1814, Ap
7	114	28.4	1203	17	US-10-650-112-27	Sequence 23153, A
8	114	28.4	1203	17	US-10-152-319A-1814	Sequence 1266, Ap
9	73	18.2	585	16	US-10-027-632-231353	Sequence 4735, Ap
10	73	18.2	585	16	US-10-027-632-231353	Sequence 24908, A
11	32	8.0	320	9	US-09-833-981-1266	Sequence 23708, A
12	12	3.5	477	10	US-09-918-975-4735	Sequence 13859, A
13	12	3.0	65	10	US-09-908-975-23708	Sequence 13870, A
14	12	3.0	312	15	US-10-029-386-23708	Sequence 13870, A
15	12	3.0	425	13	US-10-027-632-138699	Sequence 13870, A
16	12	3.0	425	13	US-10-027-632-138700	Sequence 13870, A
17	12	3.0	425	13	US-10-027-632-138701	Sequence 13870, A
18	12	3.0	425	13	US-10-027-632-138703	Sequence 138699, A
19	12	3.0	425	16	US-10-027-632-138699	Sequence 138700, A
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23	12	3.0	1056	15	US-10-029-386-10008	Sequence 419, App
24	12	3.0	1056	15	US-10-101-510-419	Sequence 1045, Ap
25	12	3.0	2271	15	US-10-101-510-419	Sequence 1045, Ap
26	12	3.0	2487	13	US-10-342-887-1045	Sequence 1045, Ap
27	12	3.0	2487	13	US-10-172-118-1045	Sequence 135, App
28	12	3.0	2725	17	US-10-205-823-135	Sequence 4009, Ap
29	12	3.0	2725	17	US-10-437-963-4009	Sequence 802, App
30	12	3.0	5181	12	US-09-968-007A-802	Sequence 83324, A
31	11	2.7	1452	17	US-10-437-963-83324	Sequence 65338, A
32	11	2.7	2190	17	US-10-437-963-91335	Sequence 3044, Ap
33	11	2.5	327	9	US-09-960-352-3044	Sequence 6254, Ap
34	10	2.5	36	9	US-09-960-352-6254	Sequence 750, App
35	10	2.5	441	9	US-10-437-963-6254	Sequence 67449, A
36	10	2.5	519	16	US-10-393-840-750	Sequence 20740, A
37	10	2.5	520	15	US-10-029-386-20740	Sequence 16847, A
38	10	2.5	543	9	US-09-864-761-16847	Sequence 24740, A
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40	10	2.5	597	9	US-09-864-761-8737	Sequence 20525, A
41	10	2.5	597	15	US-10-029-386-20525	Sequence 20688, A
42	10	2.5	642	15	US-10-029-386-20688	Sequence 64737, A
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## ALIGNMENTS

RESULT 1  
US-10-229-345-9  
; Sequence 9, Application US/10229345  
; Publication No. US20040038220A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKWITZ, Sanford D.  
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS  
; FILE REFERENCE: CWRU-P01-003  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 1209  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1161) .. (1161)  
; OTHER INFORMATION: n=a, C, G, or T  
US-10-229-345-9

Alignment Scores:







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QY 181 ArgAspProSerArgProTrrpGlyLysAspAsnTyrTrrMetLeuAsnProAsnSerGlu 200
Db 541 CGGACCCCTCGGGCGCTGGGGCAAGGACAACTACTGATGCTCAACCCCAACAGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgGlyAsnArgLeuSerHisArgAlaPro 220
Db 601 TACACTTCGCGGACGGGGGTCCTCCGCGCGCGCGAGAGGCTTCAGACCCAGCGCGCGC 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCGCTGCGCGCGCGAGGAGCCCGCGCTCCCGCGCGCGCGCGCC 720
QY 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGluGluAlaArgAla 260
Db 721 GGCGCGCGCGCGCGCGCTGCGCGCGCATGCTCCCGCGCGCGCGCGAGAGAGCGCGCC 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaAlaAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGCGCGCAAGTTCCTCAGCTCCTTCGCCATGACAGCATCCTGCGCAAGCCCTTC 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrIleGluGlnTrrpGlyAlaAlaPro 300
Db 841 CGCAGCGCTGCGCTCAGGAGCACGGCGCCCGCGAGCGCTTCAGTGGGCGCGCGCGCC 900
QY 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
Db 901 TGCCCGCGCGCTGCGCGCTTCCCGCGCTCTCCCGCGCGCGCTGCAAGGCGCTGCTG 960
QY 321 ProLeuCysAlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGlyAlaGlyVal 340
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QY 361 LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380
Db 1081 CTCGAGGCGCGCGCGCGCGCGCGCGCGCATCTGACTGCGCGCGCGCGCGCGCGAGCC 1140
QY 381 LeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSerTyrProValGluThrLeu 400
Db 1141 CTGAGAGCGCGCTTACGTCGACGCTGCGCGCGCGCGCGCGCGCGCGTGTGAGAGCCCTC 1200
QY 401 LeuAla 402
Db 1201 CTAGCT 1206

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RESULT 4
US-10-650-112-9
; Sequence 9, Application US/10650112
; Publication No. US2004010712A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CMU-001-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1161)..(1161)

```

```

; OTHER INFORMATION: n is a,t,c,g or c
US-10-650-112-9
Alignment Scores:
Pred. No.: 0
Score: 402.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 17 Gaps: 0

```

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US-10-087-080-32 (1-402) x US-10-650-112-9 (1-1209)
```

```

QY 1 MetLysLeuGluValPheValProArgAlaAlaHisGlyAspLysGluGlySerAspLeu 20
Db 1 ATGAAGTTGAGAGGTGTTTCGTCCTCCGCGCGCGCCACAGGGAGCAAGCAGGCACTGACCTG 60
QY 21 GluGlyAlaGlyLysSerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db 61 GAGGCGCGCGCGCGAGCGACGCGCGCTCCCGCTGCGCGCGCGAGAGCACTCCCTG 120
QY 41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyGlyAlaArgAspThrGln 60
Db 121 GGCTCAGATGGGACTGCGCGCGCAAGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 GlyAspGlyGluGlnSerAlaGlyGlyProGlyAlaGluGluAlaIleProAlaAla 80
Db 181 GCGCAGCGCGCAACAGAGTGGGAGGCGCGCGCGCGCGCGCGCGCGAGAGGATCCCGCAGCA 240
QY 81 AlaAlaAlaAlaValValAlaGluGlyAlaGluAlaGlyValAlaGlyProGlyAlaGly 100
Db 241 GCTGCTGACAGCGGTGGTGGCGGAGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 101 GlyAlaGlySerGlyGluGlyAlaArgSerLysProTyrThrArgArgProLysProPro 120
Db 301 GCGCGGGAGAGCGCGAGGCTGACCGAGCAAGCATATACGGCGCGCGCGCGCGCGCGCG 360
QY 121 TyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyIleArgLeuThr 140
Db 361 TACTCGACATCGCGCTCATCGCATGCGCATCGCGCATCGCGCGCGCGCGCGCGCGCGCG 420
QY 141 LeuAlaGluIleAsnGlyTyrLeuMetGlyLysPheProPheAlaGlySerTyrThr 160
Db 421 CTGGCGGAGATCAACGAGTACCTCATGGGCAAGTTCCCTTTTCCCGCGCGCGCGCGCG 480
QY 161 GlyTyrArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValIleValLeu 180
Db 481 GGTGGCGCAACTCGTCCGCGCACACCTTTCGCTCAACGACTGCTTCGTCAGAGTGTG 540
QY 181 ArgAspProSerArgProTrrpGlyLysAspAsnTyrTrrMetLeuAsnProAsnSerGlu 200
Db 541 CGGACCCCTCGGGCGCTGGGGGCAAGGACAACTACTGATGCTCAACCCCAACAGCGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgGlyAsnArgLeuSerHisArgAlaPro 220
Db 601 TACACTTCGCGGACGGGGTCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCGCTGCGCGCGAGGAGCCCGCGCTCCCGCGCGCGCGCGCGCC 720
QY 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGluGluAlaArgAla 260
Db 721 GGCGCGCGCGCGCGCGCTGCGCGCGCATGCTCCCGCGCGCGCGCGCGAGAGAGCGCGCC 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaAlaAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGCGCGCAAGTTCCTCAGCTCCTTCGCCATGACAGCATCCTGCGCAAGCCCTTC 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrIleGluGlnTrrpGlyAlaAlaPro 300
Db 841 CGCAGCGCTGCGCTCAGGAGACAGCGCGCGCGAGACAGCGCTTCAGTGGGCGCGCGCGCC 900

```

QY 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320  
 Db 901 TGCCCGCGCTGCCCGCTCCCGCTCCCGCGCGCTCCCGCGCGCTCCCGCGCGCTCCG 960  
 QY 321 ProLeuCysAlaTyrglyAlaGlyAlaProAlaArgLeuGlyAlaArgGlyAlaGlyVal 340  
 Db 961 CCGCTGCGCGTACGGCGCGGAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGG 1020  
 QY 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaPro 360  
 Db 1021 CCACCGACCGCGCGCTCCCTGCTGCACTCTCCCGCGCGCGCGCGCGCGCGCGCG 1080  
 QY 361 LeuArgGlyProAlaAlaGlyAlaAlaHisLeuTyrglyProLeuAlaGlyLeuProAla 380  
 Db 1081 CTCGAGCG 1140  
 QY 381 LeuGlnAlaAlaLeuValaArgArgProGlyProHisLeuSerTyrglyProAlaGly 400  
 Db 1141 CTCGAGCGCGCTTACG 1200  
 QY 401 LeuAla 402  
 Db 1201 CTAGCT 1206

## RESULT 5

US-10-650-112-25  
 ; Sequence 25, Application US/10650112  
 ; Publication No. US20040110712A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MARKOWITZ, Sanford D.  
 ; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS  
 ; FILE REFERENCE: CWRU-P01-044  
 ; CURRENT APPLICATION NUMBER: US/10/650,112  
 ; CURRENT FILING DATE: 2003-08-26  
 ; PRIOR APPLICATION NUMBER: 10/274,177  
 ; PRIOR FILING DATE: 2002-10-18  
 ; PRIOR APPLICATION NUMBER: 10/229,245  
 ; PRIOR FILING DATE: 2002-08-26  
 ; PRIOR APPLICATION NUMBER: 60/406,296  
 ; PRIOR FILING DATE: 2002-08-27  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 25  
 ; LENGTH: 1212  
 ; TYPE: DNA  
 ; ORGANISM: HUMAN FOXQ1  
 US-10-650-112-25

## Alignment Scores:

Pred. No.: 1,54e-291 Length: 1212  
 Score: 324.00 Matches: 324  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 80.60% Indels: 0  
 Gaps: 0

US-10-087-080-32 (1-402) x US-10-650-112-25 (1-1212)

QY 61 GlyAspGlyGlnGlnSerAlaGlyGlyProGlyAlaGlnGlnAlaLeuProAlaAla 80  
 Db 184 GGCAGCGCGCAAGAGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 243  
 QY 81 AlaAlaAlaAlaAlaAlaAlaGlnGlyAlaGlnGlyAlaGlnGlyAlaGlnGlyAlaGly 100  
 Db 244 GCTCTGAGCGGAGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 303  
 QY 101 GlyAlaGlySerGlyGlnGlyAlaArgSerTyrglyThrArgArgProGlyProPro 120  
 Db 304 GCGCGCGGAGCGCGGAGGAGTGCACGCGCAAGCACTTACGCGCGCGCGCGCGCGCGCG 363  
 QY 121 TyrglyTyrglyAlaAlaLeuAlaAlaMetAlaAlaLeuArgAspSerAlaGlyAlaArgLeuThr 140  
 Db 364 TACTGATGATCGGCTATCGCCATGCGCATCGCGCATCGCGCGCGCGCGCGCGCTTACG 423

QY 141 LeuAlaGlnLeuLeuGlnGlyTyrglyMetGlyTyrglyPheProPheAlaArgGlySerTyrglyThr 160  
 Db 424 CTGGCGGAGATCAACGAGTACTCATGGGCAAGTCCCTTTTCCCGGAGCTTACACG 483  
 QY 161 GlyTyrglyAsnSerValaGlnHisAsnLeuSerLeuAsnAspCysPheValLeu 180  
 Db 484 GGTGGCGCAACTCCG 543  
 QY 181 ArgAspProSerArgProTyrglyTyrglyAspAsnTyrglyMetLeuAsnProAsnSerGly 200  
 Db 544 CGGACCCCTCG 603  
 QY 201 TyrglyThrPheAlaAspGlyValaPheArgArgArgArgGlySerGlySerHisArgAlaPro 220  
 Db 604 TACACCTTGGCGAGCGGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 663  
 QY 221 ValProAlaProGlyLeuArgProGlyGlnGlnAlaProGlyLeuProAlaAlaProProPro 240  
 Db 664 GTCCCG 723  
 QY 241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGlnGlnArgAla 260  
 Db 724 GCG 783  
 QY 261 SerProAlaGlyTyrglyPheSerSerSerPheAlaAlaAspSerLeuLeuArgGlyProPhe 280  
 Db 784 AGCCCGCGGAGAGTCTCCAGCTCTTCCGATCGACGATCCTCGCGCAAGCCCTTC 843  
 QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyTyrglyThrLeuGlnTyrglyAlaAlaPro 300  
 Db 844 CCGAGCGCGCGCTCAGGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 903  
 QY 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320  
 Db 904 TGCCCGCGCTGCCCGCTCCCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 963  
 QY 321 ProLeuCysAlaTyrglyAlaGlyAlaProAlaArgLeuGlyAlaArgGlyAlaGlyVal 340  
 Db 964 CCGCTGTGCGTACG 1023  
 QY 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaPro 360  
 Db 1024 CCACCGACCGCA 1083  
 QY 361 LeuArgGlyProAlaAlaGlyAlaHisLeuTyrglyCysProLeuArgLeuProAlaAla 380  
 Db 1084 CTCGAGCG 1143  
 QY 381 LeuGlnAlaAla 384  
 Db 1144 CTGACGCGCGCG 1155

## RESULT 6

US-10-650-112-26  
 ; Sequence 26, Application US/10650112  
 ; Publication No. US20040110712A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MARKOWITZ, Sanford D.  
 ; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS  
 ; FILE REFERENCE: CWRU-P01-044  
 ; CURRENT APPLICATION NUMBER: US/10/650,112  
 ; CURRENT FILING DATE: 2003-08-26  
 ; PRIOR APPLICATION NUMBER: 10/274,177  
 ; PRIOR FILING DATE: 2002-10-18  
 ; PRIOR APPLICATION NUMBER: 10/229,245  
 ; PRIOR FILING DATE: 2002-08-26  
 ; PRIOR APPLICATION NUMBER: 60/406,296  
 ; PRIOR FILING DATE: 2002-08-27  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 26  
 ; LENGTH: 1203

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/ TYPE: DNA
/ ORGANISM: MOUSE FOXQ1
US-10-650-112-26

Alignment Scores:
Pred. No.: 2.83e-96      Length: 1203
Score: 114.00           Matches: 114
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 28.36%             Indels: 0
DB: 17                    Gaps: 0

US-10-087-080-32 (1-402) x US-10-650-112-26 (1-1203)

QY 105 GtGtAGGGGGCGCGGCGAGCAAGCCGTACAGCGCGCGCCCAAGCCCCCTACCTCAACATC 124
DB 304 GCGAGAGGGCGCGCGAGCAAGCCGTACAGCGCGCGCCCAAGCCCCCTACCTCAACATC 363
QY 125 AAlaLeuIleAlaMeAlaIleArgAspSerAlaGlyArgLeuThrLeuAlaGluIle 144
DB 364 GCCTCATGCGCATGGCCATCCGCACTCCGCGGCGAGCCTTGACACTGGCCGAGATC 423
QY 145 AasnGluTyrLeuMetGlyLysPheProPheArgGlySerTyrThrGlyTyrArgAsn 164
DB 424 AACGAGTACTCATGGGCAAGTCCCTTTTTCGGGGGCAAGCTACAGGGGCTGGCCCAAC 483
QY 165 SerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeuArgAspProSer 184
DB 484 TCCGTGCGGCGACCAACTCTGCTCAACGACTGTTGTCMAAGGTGCTGCGCGCCCTCG 543
QY 185 ArgProTyrGlyLysAspAsnTyrTyrMetLeuAsnProAsnSerGluTyrThrPheAla 204
DB 544 CGGCGCTGGGGGCAAGGACATTAAGATGCTCAACCCCAACGCAATACACTTCGCC 603
QY 205 AspGlyValPheArgArgArgArgLysArgLeuSerHisArg 218
DB 604 GACGGGGTCTTCGCGCGCGCCGCGCAAGCGCTCAGCCACCGG 645

RESULT 7
US-10-650-112-27
/ Sequence 27, Application US/10650112
/ Publication No. US20040110712A1
/ GENERAL INFORMATION:
/ APPLICANT: MARROWITZ, Sanford D.
/ TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
/ FILE REFERENCE: CWRU-P01-044
/ CURRENT APPLICATION NUMBER: US/10/650,112
/ PRIOR FILING DATE: 2003-08-26
/ PRIOR APPLICATION NUMBER: 10/274,177
/ PRIOR FILING DATE: 2002-10-18
/ PRIOR APPLICATION NUMBER: 10/229,245
/ PRIOR FILING DATE: 2002-08-26
/ PRIOR APPLICATION NUMBER: 60/406,296
/ PRIOR FILING DATE: 2002-08-27
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 27
/ LENGTH: 1203
/ TYPE: DNA
/ ORGANISM: RAT FOXQ1
US-10-650-112-27

Alignment Scores:
Pred. No.: 2.83e-96      Length: 1203
Score: 114.00           Matches: 114
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 28.36%             Indels: 0
DB: 17                    Gaps: 0

US-10-087-080-32 (1-402) x US-10-650-112-27 (1-1203)

QY 105 GtGtAGGGGGCGCGGCGAGCAAGCCGTACAGCGCGCGCCCAAGCCCCCTACCTCAACATC 124
```

```
DB 304 GGTAGGGCGCGCGGCGAGCAAGCCGTACAGCGCGCGCCCAAGCCCCCTACCTCAACATC 363
QY 125 AAlaLeuIleAlaMeAlaIleArgAspSerAlaGlyArgLeuThrLeuAlaGluIle 144
DB 364 GCCTCATGCGCATGGCCATCCGCACTCCGCGGCGAGCCTTGACACTGGCCGAGATC 423
QY 145 AasnGluTyrLeuMetGlyLysPheProPheArgGlySerTyrThrGlyTyrArgAsn 164
DB 424 AACGAGTACTCATGGGCAAGTCCCTTTTTCGGGGGCAAGCTACAGGGGCTGGCCCAAC 483
QY 165 SerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeuArgAspProSer 184
DB 484 TCCGTGCGGCGACCAACTCTGCTCAACGACTGTTGTCMAAGGTGCTGCGCGCCCTCG 543
QY 185 ArgProTyrGlyLysAspAsnTyrTyrMetLeuAsnProAsnSerGluTyrThrPheAla 204
DB 544 CGGCGCTGGGGGCAAGGACATTAAGATGCTCAACCCCAACGCAATACACTTCGCC 603
QY 205 AspGlyValPheArgArgArgArgLysArgLeuSerHisArg 218
DB 604 GACGGGGTCTTCGCGCGCGCCGCGCAAGCGCTCAGCCACCGG 645

RESULT 8
US-10-152-319A-1814
/ Sequence 1814, Application US/10152319A
/ Publication No. US20040072160A1
/ GENERAL INFORMATION:
/ APPLICANT: Mendrick, Donna
/ APPLICANT: Porter, Mark
/ APPLICANT: Johnson, Kory
/ APPLICANT: Higgs, Brandon
/ APPLICANT: Castle, Arthur
/ APPLICANT: Blaschoff, Michael
/ TITLE OF INVENTION: Molecular Toxicology Modeling
/ FILE REFERENCE: 44921-5089-US
/ CURRENT APPLICATION NUMBER: US/10/152,319A
/ PRIOR FILING DATE: 2002-05-22
/ PRIOR APPLICATION NUMBER: US 60/292,335
/ PRIOR FILING DATE: 2001-05-22
/ PRIOR APPLICATION NUMBER: US 60/297,523
/ PRIOR FILING DATE: 2001-06-13
/ PRIOR APPLICATION NUMBER: US 60/298,925
/ PRIOR FILING DATE: 2001-06-19
/ PRIOR APPLICATION NUMBER: US 60/303,810
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/303,807
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/303,808
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/315,047
/ PRIOR FILING DATE: 2001-08-28
/ PRIOR APPLICATION NUMBER: US 60/324,928
/ PRIOR FILING DATE: 2001-09-27
/ PRIOR APPLICATION NUMBER: US 60/330,867
/ PRIOR FILING DATE: 2001-11-01
/ PRIOR APPLICATION NUMBER: US 60/330,462
/ PRIOR FILING DATE: 2001-10-22
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2221
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1814
/ LENGTH: 1760
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. NM_022858
US-10-152-319A-1814

Alignment Scores:
Pred. No.: 3.9e-96      Length: 1760
Score: 114.00           Matches: 114
Percent Similarity: 100.00%      Conservative: 0
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 28.36% Indels: 0  
DB: 12 Gaps: 0  
US-10-087-080-32 (1-402) x US-10-152-319A-1814 (1-1760)

QY 105 GYLYGLUAGLALAGSERLYSPROTCTHARGARPROLYSPROPTOTYRSETYRILE 124  
DB 508 GGTAGAGGCGCGCCACAGCCCTHACAGCGGCGCCCAAGCCCCCTCTACTCTACATC 567  
QY 125 ALALEU1LEALAWETALAILAARGASPERALAGLYLYARGLUETHRLAALAGLU1LE 144  
DB 568 GCATCTATCGCCATGAGCATCCGAGACTCCGCGCGCGAGCGCTGAGCGTCCGAGATC 627  
QY 145 ASNGLYUTLEUWETGLYLYSPHEPROPHARGLYSEYRTHRG1YTPARGASN 164  
DB 628 AAGAGATCCTCATGAGCAAGTTCCTTTTCGCGGAGCAGTACACAGGCGCTGCGGAC 687  
QY 165 SERVALARGHISASNSEUSERLEUASNAPCYSPHEVALYLVALLUENAGAAPPROSER 184  
DB 688 TCGGTGGCCACAACTCTGCTCAACAGACTGTTGTCAAGGTGCTGCGCGACCCCTCG 747  
QY 185 ARGPTCTGGLYLYSASPANITYRTPMETLEUASNPROASNSEYRTHRG1YTPARGA 204  
DB 748 CGGCGCTGGGCGCAAGACATTACTGATGCTCAACCCCAACGCAATACCTTGCC 807  
QY 205 AASGLYVALPHEARGARGARGARGLYSARGLEUSERHISARG 218  
DB 808 GACGGGGTCTTCGCGCGCGCGCAAGCGCTCAGCACCGG 849

RESULT 9  
US-10-027-632-231353/c  
; Sequence 231353, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231353  
; LENGTH: 585  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-231353

Alignment Scores:  
Pred. No.: 2.06e-58 Length: 585  
Score: 73.00 Matches: 120  
Percent Similarity: 98.36% Conservative: 0  
Best Local Similarity: 98.36% Mismatches: 1  
Query Match: 18.16% Indels: 2  
DB: 13 Gaps: 0  
US-10-087-080-32 (1-402) x US-10-027-632-231353 (1-585)

QY 264 GYLYSPHESESERPHEA1A1EASPERILLEUARGLYSPROPHARGSERARG 283  
DB 583 GGCAAGTCTCCAGCTCTCTGCGCATGACAGATCTCTGGCAAGCCCTTCGCAAGCGC 524  
QY 284 ARGLEUARGASPTHRALAPROGLYTHTRLEUGLINTRPGLYLA1A1APROCYSPRO 303  
DB 523 CGCCTCAGGAGACAGGCCCCCGGAGAGAGCTTCAAGTGGGCGCGCCCTGCGCCGCG 464  
QY 304 LEUPROALAPHEPROALALEUENUPROALALAPROCYSPROCYSPROCYSPRO 323  
DB 463 CTGCGCGGTTCCTCCGCGCTCTCCCGCGCGCCCTGCGAGGCGCTGCTGCGCTGCG 404  
QY 324 ALATYRGLYALAGLYGUPROALARGLEUGLYVALARGLUVALAGLUVALPROPTH 343  
DB 403 GCGTACGGCGCGGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 345  
QY 343 VALAPROPROLEUENLEUENALAPROLEUPROALALAPROALALAPROALALAPRO 363  
DB 344 CGCGCGCGCGCTCTGCTGACCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 285  
QY 363 YPROALALAGLYLYALAHISLEUTRYCSPROLEUARGLEUPROALALALEUENAL 383  
DB 284 CCGCGCGCGCGCGCGCGCGCGCACTGTACTGCCCCCTGCGCGCTGCGCGCGCGCG 225  
QY 383 AALA 384  
DB 224 GGCC 221

RESULT 10  
US-10-027-632-231353/c  
; Sequence 231353, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231353  
; LENGTH: 585  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-231353

Alignment Scores:  
Pred. No.: 2.06e-58 Length: 585  
Score: 73.00 Matches: 120  
Percent Similarity: 98.36% Conservative: 0  
Best Local Similarity: 98.36% Mismatches: 1  
Query Match: 18.16% Indels: 2  
DB: 16 Gaps: 0  
US-10-087-080-32 (1-402) x US-10-027-632-231353 (1-585)

QY 264 GYLYSPHESESERPHEA1A1EASPERILLEUARGLYSPROPHARGSERARG 283  
|||||

Db 583 GGCAAGTTCTCCAGCTCTTGGCCATCGACAGCATCTGCGCAAGCCCTTCGGCAGCCGC 524  
Qy 284 ArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrrpGlyAlaAlaProCysProPro 303  
Db 523 CCCCTTCAGGAGACACGGCCCCCGGAGCAGCGCTTCAGTGGGGGGCGCGCCCTCGCCGCGC 464  
Qy 304 LeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeuProLeuCys 323  
Db 463 CTGCCCCGCTTCCCGCGCTCTCTCCCGCGGCGCTCGAGGGCCCTGCTGCGCGCTCTGC 404  
Qy 324 AlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGluAlaGlyValProProth 343  
Db 403 GGTACGGGGCGGGCGAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 345  
Qy 343 rAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysProLeuArgG 363  
Db 344 CGGGCGCGCCCTCTCTCTGACCTCTCCCGGGCGCGCGCGCGCGCGCGCGCGCGCGC 285  
Qy 363 yProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAlaLeuGlnAl 383  
Db 284 CCGGGC 225  
Qy 383 aAla 384  
Db 224 GGCC 221

## RESULT 11

US-09-833-381-1266  
; Sequence 1266, Application US/09833381  
; Patent No. US20020132090A1  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: 09/516,448  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1266  
; LENGTH: 320  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) - (320)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-1266

## Alignment Scores:

Pred. No.: 1.65e-20 Length: 320  
Score: 32.00 Matches: 45  
Percent Similarity: 97.83% Conservative: 0  
Best Local Similarity: 97.83% Mismatches: 0  
Query Match: 7.96% Indels: 1  
DB: 9 Gaps: 0

US-10-087-080-32 (1-402) x US-09-833-381-1266 (1-320)

Qy 220 ProValProAlaProGlyLeuArgProGlnGluAlaProGlyLeuProAlaAlaProPro 239  
Db 92 CCGGTCGCCCGCGCGCGGCTCGGCGCGAGGAGCGCCCGGGCTCTCCCGCGCGCGCGCN 151  
Qy 240 ProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGlnGlu 259  
Db 152 CTTCCGCGCGCGCGCGCGCGCGCTCGCGCATGCGCTGCGCGCGCGCGCGAGAGCG 211  
Qy 259 GAlaSerProAlaGly 264  
Db 212 CGCCAGCGCGCGCGCGCGC 227

## RESULT 12

US-09-918-995-4735  
; Sequence 4735, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hysq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4735  
; LENGTH: 477  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) - (477)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-4735

## Alignment Scores:

Pred. No.: 0.00126 Length: 477  
Score: 14.00 Matches: 14  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.48% Indels: 0  
DB: 10 Gaps: 0

US-10-087-080-32 (1-402) x US-09-918-995-4735 (1-477)

Qy 118 LysProProTyrSerTyrIleAlaLeuIleAlaMetAlaIle 131  
Db 105 AAGCTCCCTACAGCTACATGCGCTTATGCTATGGCGCATC 146

## RESULT 13

US-09-908-975-24908  
; Sequence 24908, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Iliat  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24908  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-24908

## Alignment Scores:

Pred. No.: 0.0172 Length: 65  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.99% Indels: 0  
DB: 10 Gaps: 0

US-10-087-080-32 (1-402) x US-09-908-975-24908 (1-65)  
Qy 391 ProHisLeuSerTyrProValGluThrLeuLeuAla 402  
Db 3 CGGCACCTGCTCTACCGGTGAGACTGCTGCTACT 38  
RESULT 14  
US-10-029-386-23708  
; Sequence 23708, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
; FILE REFERENCE: A60MCA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; NUMBER OF SEQ. ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ. ID NO 23708  
; LENGTH: 312  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR2.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5  
; OTHER INFORMATION: SWISSPROT HIT: Q60688, EVALUATE 1.00e-58  
; OTHER INFORMATION: EST\_HUMAN HIT: AM236501.1, EVALUATE 3.00e-76  
; OTHER INFORMATION: NT HIT: U13223.1, EVALUATE 0.00e+00  
US-10-029-386-23708  
Alignment Scores:  
Pred. No.: 0.0639 Length: 312  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.99% Indels: 0  
DB: 15 Gaps: 0  
US-10-087-080-32 (1-402) x US-10-029-386-23708 (1-312)  
Qy 167 ArgHisAsnLeuSerLeuAsnAspCysPheValIys 178  
Db 158 CGGCACAACCTCTCGCTGAGACGACTGCTGCTAG 193  
RESULT 15  
US-10-027-632-138699  
; Sequence 138699, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: Polymorphisms in the Human Genome  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ. ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ. ID NO 138699  
; LENGTH: 425  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-138699  
Alignment Scores:  
Pred. No.: 0.0829 Length: 425  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.99% Indels: 0  
DB: 13 Gaps: 0  
US-10-087-080-32 (1-402) x US-10-027-632-138699 (1-425)  
Qy 167 ArgHisAsnLeuSerLeuAsnAspCysPheValIys 178  
Db 238 CGGCACAACCTCTCGCTGAGACGACTGCTGCTAG 273  
Search completed: September 2, 2004, 19:43:22  
Job time : 605 secs

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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 2, 2004, 15:09:29; Search time 96 Seconds

(without alignments)  
2323.857 Million cell updates/sec

Title: US-10-087-080-32  
Perfect score: 2123  
Sequence: 1 MKLEVFYFRAHGDQKQSD.....AALVRRPPLSLVPTTLA 402

Scoring table: BLOSUM62  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q/cgn2\_1/USPTO.spool/US10087080/runat.27082004.104031.13248/app.query.fasta\_1.583  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database:

Issued Patents NA:\*  
1: /cgn2\_6/prodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/6A.COMB.seq:\*  
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5: /cgn2\_6/prodata/2/ina/6C.COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/6D.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	22.1	320	4	US-09-833-381-1266
2	468.5	22.1	3946	3	US-09-083-351-1
3	468.5	22.1	3946	3	US-09-083-352-1
4	446.5	21.0	1965	4	US-09-220-133-21
5	425	20.0	1659	3	US-09-083-351-3
6	425	20.0	1659	3	US-09-083-352-3
7	404.5	19.1	1860	2	US-08-331-644-3
8	404.5	19.1	1860	5	PCT-US93-04102-3
9	403.5	19.0	1309	4	US-07-882-292-1
10	400.5	18.9	2830	2	US-07-882-292-1
11	400.5	18.9	2830	1	US-08-331-644-1
12	400.5	18.9	2830	5	PCT-US93-04102-1

13	360.5	17.0	1155	2	US-08-331-644-4	Sequence 4, Appli
14	360.5	17.0	1155	5	PCT-US93-04102-4	Sequence 4, Appli
15	324.5	15.3	5080	4	US-09-976-594-495	Sequence 495, App
16	309.5	14.6	1605	4	US-09-087-134-10	Sequence 10, Appli
17	307	14.5	1634	4	US-09-087-134-13	Sequence 13, Appli
18	306.5	14.4	1793	3	US-09-113-309-1	Sequence 1, Appli
19	306.5	14.4	1793	3	US-09-521-107-1	Sequence 1, Appli
20	306.5	14.4	1793	4	US-09-562-332-1	Sequence 16, Appli
21	297	14.0	1668	4	US-09-087-134-16	Sequence 1, Appli
22	264	12.4	2517	1	US-07-906-930E-1	Sequence 1, Appli
23	264	12.4	3465	4	US-09-023-655-1136	Sequence 1, Appli
24	263	12.4	2939	1	US-07-906-930E-3	Sequence 1, Appli
25	251.5	11.8	3394	4	US-09-620-312D-314	Sequence 3, Appli
26	236	11.1	3342	2	US-08-742-753-3	Sequence 3, Appli
27	233.5	11.0	3441	2	US-08-742-753-3	Sequence 3, Appli
28	231	10.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
29	229.5	10.8	4403765	3	US-09-103-840A-2	Sequence 1, Appli
30	228.5	10.8	2888	4	US-08-765-507A-1	Sequence 2, Appli
31	226	10.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
32	224	10.6	4403765	3	US-09-103-840A-2	Sequence 1, Appli
33	216	10.2	1869	4	US-09-372-668-3	Sequence 2, Appli
34	216	10.2	1869	4	US-09-697-377-3	Sequence 3, Appli
35	216	10.2	1869	4	US-09-696-868-3	Sequence 3, Appli
36	216	10.2	1869	4	US-09-697-341-3	Sequence 3, Appli
37	211.5	10.0	12001	1	US-08-458-568A-11	Sequence 11, Appli
38	210.5	9.9	2481	4	US-09-894-998A-35	Sequence 35, Appli
39	210.5	9.9	12425	4	US-09-616-289-50	Sequence 50, Appli
40	208	9.8	8438	1	US-07-945-283-1	Sequence 1, Appli
41	207.5	9.8	2150	2	US-08-318-837-1	Sequence 1, Appli
42	206.5	9.7	2561	4	US-09-616-289-48	Sequence 48, Appli
43	205.5	9.7	2109	4	US-09-370-838-153	Sequence 153, App
44	204	9.6	34094	4	US-09-292-034-1	Sequence 1, Appli
45	203	9.6	12001	1	US-08-458-568A-11	Sequence 11, Appli

## ALIGNMENTS

RESULT 1  
US-09-833-381-1266  
; Sequence 1266, Application US/09833381  
; Patent No. 6672186  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1266  
; LENGTH: 320  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(320)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-1266

## Alignment Scores:

Pred. No.: 1.09e-17 Length: 320  
Score: 470.00 Matches: 94  
Percent Similarity: 89.62% Conservative: 1  
Best Local Similarity: 88.68% Mismatches: 9  
Query Match: 22.14% Indels: 2  
DB: 4 Gaps: 0

US-10-087-080-32 (1-402) x US-09-833-381-1266 (1-320)

Qy 190 AspsnYrTTPmctLeuAsnProAsnSerGluTyrThrPheAlaAspGlyValPheArg 209



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Db 1204 GCCGCCCTGGGAGGAGGAGGCGCGCGGCTGCCCAAGATCGAGAGCCCGGAGAGAGC 1263
QY 254 ---AlaArgIngluArgAlaSerProAlaGlyLysPhe----- 266
Db 1264 AGCAGCAGCCTGTCACAGGGAGAGAGCCCGGAGAGCTCCGCTGAGCGGCGCGCTC 1333
QY 266 ----- 266
Db 1324 AGCTGAGCGGTGGGATTCCGCGCGCGCGCGCGCGCTCCGCGCGCGCGCGAGC 1393
QY 267 ---SerSerSerPheAlaIleAspSerIleLeuArgLys----- 278
Db 1384 CATAGCCAGGGCTTCACGCTGAGACATCATGACGCTGCGGGGGGTGCGCGAGAGC 1443
QY 279 -----ProPheArgSerArgArgLeuArgAspThrAlaProG1 291
Db 1444 GCGGCGCGGAGAGCTACGCTCCGCGCTTCGCGCTCGCGCGCGCGCTCCGCGCGG 1503
QY 291 YThrThrLeuGlnTyrGlyAlaAlaProCysProProLeuProAlaPheProAlaLeu 311
Db 1504 ATGCGACCCCGCGTGGCTGCGCGCTTACCTCGCGCGCGAGAGCTCCCTTACAGCTCC 1563
QY 311 uProAlaAla-----ProCysArgAlaLeuLeuProLeuCysAlaTyrGlyAlaGly1 329
Db 1564 CCTGAGCGCAGACCTTCACGCGCGCGAGCTCGGGCGCGCGCGCGCGCGCGCGG 1623
QY 329 uProAlaArgLeuGlyAlaArgGluAlaGluValProProThrAla-----ProPr 346
Db 1624 G-----CGGGGGCGCGCGCGCGCGCGCGCGAGACTTGCACCTGCAAGCCATG 1674
QY 346 oLeuLeuLeuAlaProLeu-----ProAlaAlaAlaPr 357
Db 1675 AGCCTGTACCGCGCGCGCGAGCGCGCGCGCGCGCTTGCAGAGCGCGCGCGCGG 1734
QY 357 oAlaLysProLeuAlaArgGlyProAlaAlaGlyAlaHisLeuTyrCysPro----- 374
Db 1735 GGGTCGCGCGGTGACCAACCCCG-----TGCCGCACTACTCT 1770
QY 375 ---LeuArgLeuProAlaAlaLeuGlnAlaAlaLeuValArgArgPro 389
Db 1771 CTGCTCTCGGTACCAAGAGCA-----GCTCGTGTCTCC 1804

RESULT 3
US-09-083-352-1
; Sequence 1, Application US/09083352
; Patent No. 6207450
; GENERAL INFORMATION:
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Stone, Edwin M.
; APPLICANT: Nishimura, Darryl
; APPLICANT: Pacil, Shiva
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,352
; FILING DATE: 22-MAY-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

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; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-029.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3946 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 475..2133
; US-09-083-352-1

Alignment Scores:
Pred. No. 1 87e-16 Length: 3946
Score: 468.50 Matches: 165
Percent Similarity: 38.92% Conservative: 44
Best Local Similarity: 30.73% Mismatches: 143
Query Match: 22.07% Indels: 186
DB: Gaps: 23

US-10-087-080-32 (1-402) X US-09-083-352-1 (1-3946)
QY 8 ProArgAlaAlaHisGlyAspLysGlnGlySerAspLeuGluGlyAlaGlyLysSerAsp 27
Db 287 CCGAGGCGCGCGAGAGAGCCCGCGAGCGCGCGCGAGAGCGCGCGAGAGCGCGAGC 346
QY 28 Ala-----ProSerProLeuSerAlaAlaGlyAspAspSerLeuGlySerAsp 43
Db 347 GCACAGCGCAGCGCGCGCGAGCA---GCTCGCGCGCGCGCGAGACTCGCGCGCGCC 403
QY 44 GlyAspCysAlaAlaLysProSerAlaGlyGlyAlaAlaArgAspThrGlnGlyAspGly 63
Db 404 GCGCGCGCGCGCGCGCGCGCGCGAGCGAGGTGGGGCGCGCGCGCGCGCGCGCGCG 463
QY 64 GluGlnSerAlaGlyGlyGlyProGlyAlaGluGluAlaLeuProAlaAlaAla----- 81
Db 464 GAGCGG-----GCGGCA---TGAGGCGCGCTACTCTCGTGTCCAGGCCCAACT 508
QY 82 -----AlaAlaAlaValAlaAlaGluGlyAlaGluAlaGly 93
Db 509 CCTGTGAGTGTGCTTACTCTCGCGCGAGAGAGTACTACCGC-GCGGCGCGCG 567
QY 94 AlaAlaGlyProGly----- 98
Db 568 GCGGCGCGGGGCGGCTTACCGCCATCGCGCGCGCGCGCGCGCGCGTGTACTCGCACCTGCG 627
QY 99 -----AlaGlyGlyAlaGlySerGlyGluGlyAlaArgSerLysProTyr 113
Db 628 CACGCGAGCAGTACCGCGCGCGCATGCGCGCGCTTACGCG-----CCCTAC 675
QY 114 ThrArgArgPro-----LysProProTyrSerTyrIleAlaLeu 127
Db 676 ACGCGCGAGCCCGAGCGCAAGAGATGGAAGCCGCTTATAGTACTACGCGCTCATC 735
QY 128 AlaMetAlaIleArgAspSerAlaGlyArgLeuThrLeuAlaGluIleAsnGluTyr 147
Db 736 ACCATGTGCATCCAGAGCGCGCGGAGCAAGAGATCCTTGAACGCGCATCTACAGTTTC 795
QY 148 LeuMetGlyLysPheProPhePheArgGlySerTyrThrGlyTyrArgAsnSerValArg 167
Db 796 ATCATGAGACCGCTTCCCTTCTTACCGGAGCAACAAGAGGCGTGGAGAAAGCATCCGC 855
QY 168 HisAsnLeuSerLeuAspCysPheValLysValLeuArgAspProSerArgProTyr 187
Db 856 CACAACCTCTGCTCAACAGGTCTTCGCAAGGTGCGCGCGAGCAAGAACGCG--- 912
QY 188 GlyLysAspAsnTyrTyrMetLeuAsnProAsnSerGluTyrThrPheAlaAspGlyVal 207

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Db      913 GCGAAGGCGACGCTTCTGAGCGTGGACCGGACCTCTCAACAATGTTTCAGAAAGCGAGC 972
Qy      208 PheArgArgArgArgArgArgSerHis----- 217
Db      973 TTCTCGGGGGGGGGGGCGCTTCAAGAGAGAGACCGGTTGAAGAGACAGAGAGAG 1032
Qy      218 -----ArgAlaProValProAlaProGly 225
Db      1033 GACAGGCTGACCTCAAGAGACCGCCCGCCGCGCCAGACCGCCCGCGCGCG-- 1089
Qy      226 LeuArgProGluGluAlaProGlyLeuProAlaAlaPro----- 238
Db      1090 -----CCGAGACGAGCGCGAGCGGCGCGCGCTCCGAGCGCGCGCGCGCGATC 1143
Qy      239 -----ProProAlaProAlaAlaProAla 246
Db      1144 CAGGACATCAAGACCGAGAACGTAAGTCCCTCGCGCGCGCGCGCGCGCGCGCG 1203
Qy      247 Ser-----ProArgMetArgSerPro----- 253
Db      1204 GCCCGCTGGGACGCGGACGCGCGCGCGCGGTGCGCCAGATCGAGAGCCCGACAGCAGC 1263
Qy      254 ---AlaArgGluGluGluArgAlaSerProAlaGlyLysPhe----- 266
Db      1264 AGCAGACGCTCTCCAGCGGAGAGACCGCCCGGAGACCTGCGCGCGCGCGCGCTC 1323
Qy      266 ----- 266
Db      1324 AGCGTGAAGGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAC 1383
Qy      267 ---SerSerSerPheAlaIleAspSerIleLeu-ArgLys----- 278
Db      1384 CATAGCCAGGCGCTTCAGCGTGAACAACATCAATGAGTGTGCGCGGGGTGCGCCGACAGC 1443
Qy      279 -----ProPheArgSerArgArgLeuArgAspThrAlaProGly 291
Db      1444 GCGCGCGGAGCTCAGCTCCGCGCTTGTGCGCTCGGCGCGCGCGCTCTCGCGCGCGGG 1503
Qy      291 YThrThrLeuGluThrGlyAlaAlaProCysProProLeuProAlaPheProAlaLeuLe 311
Db      1504 ATCGACACCGCGCTGCGCGCTGCGCTACTGCGCGCGAGAGCTCCCTCTACAGCTCC 1563
Qy      311 uProAlaAlaAla-----ProCysArgAlaLeuLeuProLeuCysAlaArgLysGly 329
Db      1564 CCTGCGACCGACCTCCAGCGCGCGGAGCTCGGCGCGCGCGCGCGCGCGCGCGCGCC 1623
Qy      329 uProAlaArgLeuGlyAlaArgGlyAlaGlyValProProThrAla-----ProPr 346
Db      1624 G-----CGGGGGGGCGCGCGCGCGCGCGAGCTTACACTGCAACCTGCAAGCTAG 1674
Qy      346 OleuLeuLeuAlaProLeu-----ProAlaAlaAlaPr 357
Db      1675 AGCTGTGACGCGCGCGGAGCGCGGGGCCACTTGCAGGGCGCGCGCGGGGGCGCGGC 1734
Qy      357 AlaAlaArgProLeuArgGlyProAlaAlaGlyAlaHisLeuTyrcysPro----- 374
Db      1735 GGTCTGGCGCGTGAACAACCC-----TGCCCACTACTCT 1770
Qy      375 ---LeuArgLeuProAlaAlaLeuGluAlaLeuValArgArgPro 389
Db      1771 CTGCTCTCGGTCAACAGAGCA-----GCTCGTCTGCTCC 1804

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; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-220-132-21

Alignment Scores:
Pred. No.: 1,31e-15 Length: 1965
Score: 446.50 Matches: 150
Percent Similarity: 44.55% Conservative: 42
Best Local Similarity: 34.80% Mismatches: 121
Query Match: 21.03% Indels: 120
Gaps: 19

US-10-087-080-32 (1-402) x US-09-220-132-21 (1-1965)
Qy      28 AlaProSerProLeuSerAlaAlaGlyAspAspSerLeuGlySerAspGlyAspCysAla 47
Db      13 GCGCGGAGACACACTCTCTCTCC-----TCGTCTGCTCTCTCGCTCTCTCGCGCC 63
Qy      48 AlaArgProSerAlaGlyGlyAlaArgAspThrGluArgGlyGluGluSerAla 67
Db      64 TCGTCTGCTCTCTCTCTCAATTCGCGC----- 90
Qy      68 GlyGlyGlyProGlyAlaGluGluAlaIleProAlaAlaAlaAlaAlaValAlaAla 87
Db      91 -----AGCGCCCTCGGCTGCTCGAG----- 114
Qy      88 GluGlyAlaGluAlaGlyAlaAlaGlyProGlyValaGlyAlaGlySerGlyGlyGly 107
Db      115 -----AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGCGCGCC 156
Qy      108 AlaArgSerLysProTyThrArgArgPro-----LysProProTyThrArgSerTyrl 126
Db      157 AAGAGGCGAGCTCGGGGCTCGCGCGCGCGCGCGAGAGCGCGCTTCTGTAATCGCGCTC 216
Qy      127 IleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThrLeuAlaGluIleAsnGlu 146
Db      217 ATCGTCAATGCGCATTCAGAGCTCCGCCAGAGCGCGCTGACGCTCAAGAGATCTAACAG 276
Qy      147 TyrlLeuMetGlyLysPheProPhePheArgGlySerTyThrGlyTyThrArgAsnSerVal 166
Db      277 TTCTCTGAGGCGCGCTCTCTCTCTCTCGCGCGCGCTTACAGAGGCTGGAAGAACTCGGTTG 336
Qy      167 ArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeuArgAspProSerArgPro 186
Db      337 GCGCAAACTCTCTCTCAAGAGCTTCTTCAAGCTGCTCAAGAGGCTCGGGGGCGCC 396
Qy      187 TrpGlyLysAspAsnTyrlTrpMetLeuAsnProAsnSerGlyTyThrPheAlaAspGly 206
Db      397 ---GCCAAGGGCGACTACTGAGCACTGAGCCCGGACGAGTATGATGTCAGAGAGGCGC 453
Qy      207 ValPheArgArgArgArgLysArgLeuSerHisArgAlaPro-----Val 221
Db      454 TCGTTCGCCCGCGCGCGC-GCGCGGCTTCAAGCGGAGAGTGCAGGGGCTCAAGCCATGTA 512
Qy      222 Pro-----AlaProGlyLeuArgPro 228
Db      513 CCACCGCGTGTGAGCGGCTTGGGCTTGGGGCGTCTGCTGCTGCTCCAGAGGCTTGA--- 569
Qy      229 GluGluAlaProGlyLeuProAlaAlaProProProAlaProAlaAlaProAlaSerPro 248
Db      570 -----CTTCCAGGCGCGCGCGCGCGCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
Qy      249 ArgMetArgSerPro-----AlaArgGluGlu 257

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Db	615	CGGCTACGGCGGCGCTTCGATCATGATGCCCGGGCGGTACACGCGCGGCGCGGCCCCCGAC	674
QY	258	GIuAa'gAla-----SerProAlaGlyuysPheSerSerSer	269
Db	675	CCACCGCGACCTTCACACCAACCAACCAACCAACGATCCGACACATGTGCCCCACACCCGGG	734
QY	270	PheAlaIleAspSerIleLeu-----ArgIysProPheArg	281
Db	735	TTTCACCTACATGGCCAGCTGCGCCGGTCCCGGGACCCGGGGCGGTGTGGTGGCGGCGG	794
QY	282	SeArGArGLeuArg-AspThrAlaProGlyIhTrhLeuGlnINTpGlyAlaAlaProCys	301
Db	795	GGCGGGCGGCGCGCGCGACTACGGGCGGACAGCAGC-----AGCAGCCGGT	842
QY	301	sProProLeuProAlaPhe-----ProAlaLeuLeuProAl	313
Db	843	ACCCCTGTCGCCGGGCATGGGAGGCGCATGCATGCCACTGCGCCCTTACACGAGCCCTGC	902
QY	313	AlaA-----ProCysArgAlaLeuLeuPro-----LeuCysAlaTyrlG	326
Db	903	GGCGCACTGAGCTCGCCTGG-CGCGCTGCCTTACTCACAAGCGCGCGCTGCCGACGC	961
QY	326	yAlaGlyLubProAlaArgLeuGlyAlaArgGlnAlaGlnAlaProProThrAlaProPr	346
Db	962	CCAGCAGCAACCCGCGCGCTTGGGAG-----CCTGCACCTCCACCATGT	1006
QY	346	OlenuLeuAlaIaProLeuProAlaAlaAlaProAlaLysProLeuArgAlaProAlaAl	366
Db	1007	CCTCCTTACGTGCTGGAGAGCAAGCTTACACACAAAGCTCG--CGAGGACCTCTGAG	1066
QY	366	aGlyGlyAlaHisLeuTyrcysProLeuArgLeuProAlaAlaLeuGlnAlaAlaLeu--	385
Db	1064	TGGGACTGCC-----CCGTACACAGCATCACTTACTCCAGAGTGTG	1106
QY	386	-ValArgArgProGlyProHisLeuSerTyrr	395
Db	1106	ACGAGAAAGATTGTCTCTCAACTTCAATGG	1136

RESULT 5  
US-09-083-351-3  
Sequence 3, Application US/09083351  
Patent No. 6087107  
GENERAL INFORMATION:  
APPLICANT: Sheffield, Val C.  
APPLICANT: Alward, Wallace L.M.  
APPLICANT: Stone, Edwin M.  
APPLICANT: Nishimura, Darryl  
APPLICANT: Patel, Shiva  
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR  
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HONG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/083,351  
FILING DATE: 22-MAY-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-029.02  
TELECOMMUNICATION INFORMATION:

```

: TELEPHONE: 617-832-1000
: TELEFAX: 617-832-7000
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1659 base pairs
: type: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-09-083-351-3

Alignment Scores:
Pred. No.: 1.51e-14
Score: 425.00
Percent Similarity: 39.91%
Best Local Similarity: 31.04%
Query Match: 20.02%
DB: 3
Length: 1659
Matches: 140
Conservative: 40
Mismatches: 112
Indels: 159
Gaps: 19

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US-10-087-080-32 (1-402) X US-09-083-351-3 (1-1659)

[illegible]

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QY      259 ArgAlaSerProAlaGlyLysPhe----- 266
      808 GGGAGCAGCCCCCGGAGCCTCGTGGCGGGCGCTCAACCTGAGCGTGGAT 867
QY      267 -----SerSerPheAla 271
      868 TCCGGCGCGCGCGCGCGCGCTCGCGCGCGCGCGCAACATAGCAGGCTTACGC 927
QY      272 IleAspSerIleLeu-ArgLys----- 278
      928 GTGGACAACATCATGACGTGCTGGGGGGTGGCGGAGCGCGCGCGAGCTCAGC 987
QY      279 ----ProPheArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrpG1 297
      988 TCCGCGCTTCTGGCTCGCGCGCGCGCGCTCTCGCGCGCGGGAGATGCAACCCCGTGGCG 1047
QY      297 YAlaAlaProCysProProLeuProAlaPheProAlaLeuLeuProAlaAla-----Pr 315
      1048 CTCGCGCGCTTACCTGCGCGCGCGAGAGTCCCTCTACAGCTCCCGCTGACGACACTCC 1107
QY      315 CCySerArgAlaLeuLeuProLeuCysAlaTyrGlyAlaGlyGlnProAlaArgLeuGlyAl 335
      1108 AGCGCGCGCGCAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG-----CGGGGGGC 1158
QY      335 aArgGluAlaGluValProProThrAla-----ProProLeuLeuLeuAlaProLe 352
      1159 GCGGGCGCGCGCGGAGCTTACCACTGCAAGCCTGAGAGCTTACCGCGCGCGCG 1218
QY      352 u-----ProAlaAlaAlaProAlaLysProLeuArgG1 363
      1219 GAGCGCGGGCGCACTTGCAGGCGCGCGCGCGCGCGCGCGCGCGCTCGCGCGTGGACAC 1278
QY      363 yProAlaAlaGlyGlyAlaHisLeuTyrCysPro-----LeuArgLeuProAl 379
      1279 CCCC-----TGCCGAGCTACTCTGCTCGCTCGGTCAACGAC 1314
QY      379 aAlaLeuGlnAlaAlaLeuValArgArgPro 389
      1315 AGCA-----GCTCGTGTCTCC 1330
Db

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RESULT 6
US-09-083-352-3
; Sequence 3, Application US/09083352
; Patent No. 6207450
; GENERAL INFORMATION:
; APPLICANT: Shefield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Stone, Edwin M.
; APPLICANT: Nishimura, Darryl
; APPLICANT: Patil, Shiva
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,352
; FILING DATE: 22-MAY-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-029.01

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1659 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-083-352-3

Alignment Scores:
Pred. No.: 1,51e-14 Length: 1659
Score: 425.00 Matches: 140
Percent Similarity: 39.91% Conservative: 40
Best Local Similarity: 31.04% Mismatches: 112
Query Match: 20.02% Indels: 159
DB: Gaps: 19

US-10-087-080-32 (1-402) x US-09-083-352-3 (1-1659)
QY      72 GlyAlaGluGluAlaIleProAlaAlaAlaAlaValAlaGluGlyAlaGlu 91
      58 GCGCGGAGCAGAGCTACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCTAC 111
QY      92 AlaGlyAlaAlaGlyProGlyAla----- 99
      112 ACCGCCATGCCGCGCGCGCGCGCTGACCGCTGACCGCGCGCGCGCGCGAGATACCG 171
QY      100 GlyGlyAlaGlySerGlyGlyAlaArgSerLysProTyrThrArgArgPro----- 117
      172 GCGCGCATGGCGCGCGCGCTACCGG-----CCCTACACGCCCGCAGCGCGAGCGCC 219
QY      118 -----LysProProTyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAsp 133
      220 AAGACATGATGTAAGCGCGCTTATGCTACATCGGCTCATCATCATGAGCATTCAGAAC 279
QY      134 SerAlaGlyGlyArgLeuThrLeuAlaGluIleAsnGlyTyrLeuMetGlyLysPhePro 153
      280 GCCCGGAGCAGAAATATCATCTGAGACGGCATCTACAGCTCATCATGAGACGCTTCCC 339
QY      154 PhePheArgGlySerTyrThrGlyTyrArgAsnSerValArgHisAsnLeuSerLeuAsn 173
      340 TTCTACCGGAGACAAACAGAGGCTGCGAGAACACATCCGCCACACCTCTCGCTCAC 399
QY      174 AspCysPheValIleValLeuArgAspProSerArgProTyrGlyLysAspAsnTyrTrp 193
      400 GAGTCTTGTCTCAAGTGGCGCGCGCGAGCAAGAACCG--GGCAAGGCGAGTACTGG 456
QY      194 MetLeuAsnProAsnSerGlyTyrThrPheAlaAspGlyValPheArgArgArgLys 213
      457 ACGCTGAGCCCGAGCTCTTACAAACATGTTGAGAACGGGAGAGCTTCTCGGGGGCGCG 516
QY      214 ArgLeuSerHis----- 217
      517 CGCTTCAAGAGAGAGAGAGCGGTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 576
QY      218 -----ArgAlaProValProAlaProGlyLeuArgProGluGluAla 231
      577 GAGCGCGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCG-----CCGAGCAGGCC 627
QY      232 ProGlyLeuProAlaAlaPro----- 238
      628 GACGGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCATCAGACATCAAGACCGAG 687
QY      239 -----ProProAlaProAlaAlaProAlaSer----- 247
      688 AACGTACGTGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 747
QY      248 -----ProArgMetArgSerPro-----AlaArgGlnGluGln 258
      748 AGCGCGCGCGCGGTGCGCAAGATCGAGAGCGCGCGCGAGCAGCAGCAGCAGCGCTGTCAGC 807

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QY 259 ArgAlaSerProAlaGlyLysPhe----- 266  
 Db 808 GGGAGACGCCCCCGGAGCCTGCTGGCGGGCGCTACGCTGAGCGGTGGGAT 867  
 QY 267 -----SerSerPheAla 271  
 Db 868 TCCGGCGCGCGCGCGCGCGCTCCGCCCCCGCGGACCATAGCAGGGCTTCAGC 927  
 QY 272 ILAspSerIleLeu-ArgLys----- 278  
 Db 928 GTGACACATCATGATGCTGCTGGGGGTGCTCGCGAGCGCGCGCGAGCTTACG 987  
 QY 279 -----ProPheArgSerIleuArgLeuArgAspThrAlaProGlyThrThrIleuGlnTrpG1 297  
 Db 988 TCCGCGCTTCTGGCTTGGCGCGCGCGCTCTCGCGCGCGGGATGCAACCCCGCTGCGG 1047  
 QY 297 yAlaAlaProCysProProleuProAlaPheProAlaLeuProAlaAla-----Pr 315  
 Db 1048 CTCGGCGCTTACTGCGCGCGCGCGAGCTCCCTCTACAGCTCCCTTCAGCGAGACCTCC 1107  
 QY 315 oCyArgAlaLeuLeuProleuCysAlaTyrGlyAlaGlyGlnProAlaArgLeuGlyAl 335  
 Db 1108 AGCGCGGGCAGCTCGGGCGGGCGGGCGGGCGGGCGG-----CGGGGGGC 1158  
 QY 335 aArgGluAlaGluValProProthAla-----ProProleuLeuAlaProle 352  
 Db 1159 GCGGGCGCGCGCGGAGCTACCTGCAACCTGCAAGCTGATGAGCTGTAGCGGGCGGCG 1218  
 QY 352 u-----ProAlaAlaAlaProAlaLysProleuArg1 363  
 Db 1219 GAGCGCGGGGCGCAGCTTGCAGGGCGCGCGCGGGCGCGCTCGCGGTGGAGCAAC 1278  
 QY 363 yProAlaAlaGlyAlaHisLeuTyrCysPro-----LeuArgLeuProAl 379  
 Db 1279 CCCC-----TCCCGAGCTACTCTCTGCTCCGCGGTACACAGC 1314  
 QY 379 aAlaLeuGlnAlaAlaLeuValArgArgPro 389  
 Db 1315 AGCA-----GCTGCTGCTCC 1330  
 RESULT 7  
 US-08-331-644-3  
 ; Sequence 3, Application US/08331644  
 ; Patent No. 5976872  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tao, Wufan  
 ; APPLICANT: Lai, Eseng  
 ; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham  
 ; STREET: 1165 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/331,644  
 ; CLASSIFICATION: 435  
 ; PRIORITY DATA:  
 ; APPLICATION NUMBER: US 07/882,292  
 ; FILING DATE: 13-MAY-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41472-A-PCT-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-278-0400  
 ; TELEFAX: 212-391-0525  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1860 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-331-644-3  
 Alignment Scores:  
 Pred. No.: 2,09e-13 Length: 1860  
 Score: 404.50 Matches: 133  
 Percent Similarity: 40.95% Conservative: 30  
 Best Local Similarity: 33.42% Mismatches: 132  
 Query Match: 19.05% Indels: 104  
 Gaps: 13  
 US-10-087-080-32 (1-402) x US-08-331-644-3 (1-1860)  
 QY 8 ProArgAlaAlaHis-----GlyAspLysGlnGlySerAspLeuGlnGly 22  
 Db 245 CCGCGCGTGCAGAGTGGCGTCTCGCTCCGGGTCCGCGCGCGGATGCGCTGGGGA 304  
 QY 23 AlAGlyGlySerAspAlaProSerProleuSerAlaAlaGlyAsp----- 37  
 Db 305 GCGCAGGAGCGCGGAGCGCGGTGCTTATGTGCGCGCGCGCACCGCGCGCGCGCCAGC 364  
 QY 38 ---AspSerLeuGlySerAspGlyAspCys----- 46  
 Db 365 TATGACCTTGAGCAGAGATGTCCGATGCTCCGGCTTCGAGAGAGACAGATCGA 424  
 QY 47 -----AlaAlaLysProSerAlaGlyGlyAlaArg-AspThrGlnGlyAspG1 63  
 Db 425 CCGGTGGGGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGATGACAGAGGGCGGCG 484  
 QY 63 yGlnGlnSerAlaGlyGlyGly----- 70  
 Db 485 CGGCGCGCGCGCGGGGTCCCGGTGGCGAGCTCGCCAGCGCGCGCGCGCGCTCTTA 544  
 QY 70 ----- 70  
 Db 545 CCGCGGAGGTCATCTTGAGACCTTGAGAGAGAGAGAGAGATGACCTGCTGCGC 604  
 QY 71 -----ProGlyAlaGlnGluAlaIleProAlaAlaAlaAlaAlaValAlaG1 88  
 Db 605 CCGCGCGCGCGCGGTCCCGCGCGCTCCGGGTCTCGCGCGCGCGCGCGCGGCTC 664  
 QY 88 uGlyAlaGluAlaGlyAla---AlaGlyProGlyAlaGly-----GlyAlaGlySe 104  
 Db 665 GGGCGCGTGCAGCGCGCGCGAGCGGAGCGCGCGGAGGTGTAACGGGCGCGGCGAC 724  
 QY 104 rGlyGlnGlyAlaArgSerLysProTyrThrArgArgProLysProProTyrSerTyr11 124  
 Db 725 GGGCGGGCGCGCTTAAGAT---CCGCTGCTG-----AAGCGCGCTTACTCTGACAT 772  
 QY 124 eAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThrLeuAlaG1 144  
 Db 773 CCGCTCATACACATGGCCATCTGCAGAGCGCCCAAGAGCGCTGACGCGAGAT 832  
 QY 144 eAsnGlyTyrLeuMetGlyLysPheProPheAlaArgGlySerTyrThrGlyTyrArgAs 164  
 Db 833 CTGCGAGTTCATACAGACCGCTTCCCTTACACCGGAGAGAGTCCCGCTTGCGAGA 892  
 QY 164 nSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeuArgAspProSe 184  
 Db 893 CAGCATCTCATCAACCTGTGCTTAAGATGCTTGTCAAGATCCCGCGGAACCGGG 952  
 QY 184 rArgProTyrGlyLysAspAsnTyrTyrMetLeuAsnProAsnSerGlyTyrThrPheAl 204







```

Db      1074 -----GGGACTCTGACCAAGGACAGCCCTGTCTCACTGTGGA 1111
Qy      264 ylypPheSerSer-SerPheAlaIleaspSerIleuAarglyProPheArgSerArga 284
Db      1112 GAACTTACTGCTAGATTT-----CCAAATTGTTAGGAAGCTGTTAGCCGCGGG 1162
Qy      284 rgleuAargApThAlaProGlyThrThrIleuGlnTrpGly-----AlaAlaProCysp 302
Db      1163 AGAGCCAGAGTAGGACTCCGGGCTTCTTCTCCGAGTGGGGGGTGTGTTCCGTGCGCC 1222
Qy      302 roProleuProAlaPheProAlaIleuProAlaIleuProCysArgAlaIleuPro- 321
Db      1223 CTCGGGCTCTCGGAGAGCCCGCGCCCGCC-CGGTTTTCGGCTTGGGATTTCTTGACCAAG 1281
Qy      322 -LeuCysAlaTyGlyAlaGlyIleuProAlaAargIleuGlyAlaArg 336
Db      1282 ACTGTGTGGGCGACAGCTGGGGGGCGGCGCACTTTAGCTCAGAGG 1327

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## RESULT 9

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US-09-976-594-927
; Sequence 927, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 927
; LENGTH: 1309
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6673549 3687719CB1
US-09-976-594-927

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Alignment Scores:
Pred. No.: 1,63e-13 Length: 1309
Score: 403.50 Matches: 135
Percent Similarity: 44.21% Conservative: 33
Best Local Similarity: 35.53% Mismatches: 136
Query Match: 19.01% Indels: 77
DB: 4 Gaps: 14

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US-10-087-080-32 (1-402) x US-09-976-594-927 (1-1309)
Qy      75 GtAlaIleProAlaAlaAlaAlaIleAlaValAlaIleGluGlyAlaGluAlaGlyAl 94
Db      4 GAAAGTGAAGCTGACCCAGAGGAGGCTCCAGCAAGCTGGGAGCCCGGCGAGATGCGAGCG 63
Qy      94 aAlaGly-ProGlyAlaGlyAlaGlySerGlyGluGlyAlaAargSerIysProTyrt 114
Db      64 AGCCTCTGCGCGGCGCTGCGCC-----CCACAA 93
Qy      114 hArGArgProlAysProProTyrtSerTyrtIleAlaIleuIleAlaMetAlaIleArgAsp 134
Db      94 CTGAGCCACCAAGCTCTCTTACAGCTACATGCGCTTATGCTATGCGCATCCAGAGCT 153
Qy      134 eAlaGlyGlyAArgIleuThrIleuAlaGluIleuAengIuTyrlleuMetGlyIysPhePro 154
Db      154 CACGGGGGACAGCGGCCACCTCTAGTGCAATTCACCGCTACATATGGCGGATTCGCT 213
Qy      154 hePheAArgGlySerTyrtThrIyTyrtPArgAenSerValArgHISAsnIleuSerIleuSna 174
Db      214 TCTACCGCCACACCGCGCGCTGGCGAGACAGCATCCGCGCACATCTGTCACTCAAGC 273

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```

Qy      174 spCysPheValIysValIleuAArgAspProSerArgProTrpGlyIysAspAsnTyrtTrpm 194
Db      274 AGTGCCTTTCATCAGAGTCCCGCGATACCGCAAGCA-----GGCAAGGCGAGCTACAGCA 330
Qy      194 etIleuSnpProAenSerGlyTyrtThrPheAlaaspGlyValPheArgArgArgIysa 214
Db      331 CGCTGACACCTGACTGCGACAGACATGTTTAGACAGCGGCACTTCTTACGCGCGCGGCC 390
Qy      214 rgleuSerHis-ArGAlaProValProAlaProGlyIleuAArgProGluGlnAla----- 231
Db      391 GCTTACCCCGGAGACAGAGTGTAGAGGACCCCGGGCGCCGCCCAAGGACGCGGTGAC 450
Qy      232 -ProGlyIleuProAla-----AlaProProProAlaProAlaIleProAla 246
Db      451 CCTCAGGGGAGGACAGCAGAGCCAGAGACTCCCAAGCGACAGCGACGAGCGAGTGT 510
Qy      247 SerProArgMetArgSerProAlaAArgGlnGluArgAla----- 260
Db      511 CATTCCACAG-----AGCTCCAGATCCCAAGGCTTAAGCTTTGGGGCTGTGG 561
Qy      261 -SerProAlaGlyIysPheSerSerSerPheAlaIleaspSerIleuAArgIysPro 279
Db      562 TGGGGGACATGCGAGCCAGATATGTCAGCAACCACTGATGAGAGCTTCGGCCACCA 621
Qy      280 PheArgSerArgArgIleuAArgAspThrAlaProGlyThrThrIleuGln--TrpGlyAla 298
Db      622 TGGAGGCCAAGAGATTT-----CCAGCGCCAGCCTGTGATGCCAGGGAGAG 669
Qy      299 AlaProCysProPro--LeuProAlaPheProAlaIleu--LeuProAla----- 313
Db      670 TCCCGGTGGCACACCTATCTTCTCA-TGCCAGGCTTTGGCTTCTGCGCGCTTCTCA 728
Qy      314 -----AlaProCysArgAlaIleuProIleuProIleuCysAlaTyrgly 326
Db      729 GAGCTGAGAGTTTAATAAGGCCCTTACGCCGCTGTGTCGCCGAATCAGGAGCTGG 788
Qy      327 AlaGlyIleuProAlaArgIleu----- 333
Db      789 AGCAGCTACAGATGTCGCTGAGGAGCACTGAATTTTGCATGGGGCTGAGCCAGGCTT 848
Qy      334 -----GlyAlaArgGluAlaGluValProProThrAlaProProIleuLeu 348
Db      849 GAGCACTCTTGGCTCAGAGAGCCCTCCCTGACAGCAACCCCTCAGAGCTCAGTCTC 908
Qy      349 LeuAlaProIleuProAlaAlaIleProAlaIysProIleuAArgIysProAlaIleGly 368
Db      909 CGGGCCCACTGCGCC-----CTGCCAACTGACCAAGAAACCTGGGTTGACAGGTGGC 962
Qy      369 AlaHisIleuTyrcysProIleuAArgIleuProAlaIleuGlnAlaIleuValArgArg 388
Db      963 TTCCTGTCAGGAGAGGCTCCGGCTTACCATTTGGGGGCTGACCCCTGCTTATCCGAGAG 1022
Qy      389 ProGly-----ProHisIleuSerTyrtProValGlu 398
Db      1023 CCAGGAATGTTCTTCTTGAATAAAGGAGGCTCAGCTCCGCGAGCTCCCTGAGC 1076

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## RESULT 10

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US-07-882-292-1
; Sequence 1, Application US/07882292
; Patent No. 5324638
; GENERAL INFORMATION:
; APPLICANT: Tao, Mufan
; APPLICANT: Lai, Eseng
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: John P. White
; STREET: c/o Cooper and Dunham, 30 Rockefeller
; CITY: New York
; STATE: New York
; COUNTRY: USA

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,292
FILING DATE: 19920513
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41472
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 42523 COOP UI
TELEX: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 443..1882
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_feature
LOCATION: 926..1255
OTHER INFORMATION: /note= "nucleotide sequence encoding DNA"
FEATURE:
NAME/KEY: binding_domain_homology
LOCATION: 1883..1885
OTHER INFORMATION: /note= "translation termination codon"
US-07-882-292-1
Alignment Scores:
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Score: 400.50 Matches: 143
Percent Similarity: 40.47% Conservative: 29
Best Local Similarity: 33.65% Mismatches: 146
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Gaps: 18
DB:
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QY 28 AlaProSerProIeu-----SerAlaIaIaGlyAsp-----AspSer 39
DB 728 ---CCCCGCGCGCTTGGCTCCCGCCGCTCCCGCCCTGACGCGGCGCAAGCTGACGCA 784
QY 40 LeuGlySerAspGlyAspCysAlaIaIaIysProSerAlaGlyGlyGlyAlaArgAspThr 59
DB 785 CTTGAGCCAAAGGCGAG-----CCAGCGCGCGGCGCTGCGGAGCTGCGCGCC 832
QY 60 GlnGlyAspGlyGlnGlnSerAlaGlyGlyGlyProGlyAlaGlnGlnAlaIleProAla 79
DB 833 GTCGGCGCGAGCGAGAGAGAGAGAGCGCGCGCTGCGGCGGAGAG----- 880
QY 80 AlaAlaIaIaIaIaIaIaIaIaIaIaGlnGlyAlaGlyAlaIaGlyProGlyAla 99
DB 881 -----AAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 907
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DB 908 GACGGGAGAGGCGGCGAGAGAGGCG-----GACAAAGAACAAAGCGCACTACGAGAGCGG 961
QY 120 ProIysSerIyrIleAlaIeuleIleAlaIeuleIaIeArgAspSerAlaGlyIyrGleu 139
DB 962 CCGTTCACCTACAGCGCGCTCATGATGCGCATACGAGAGAGCGCGAGAGCGCGCTG 1021
QY 140 ThrIeuleIaGlnIleasnGlyIyrIeuleuIeuleGlyIysPheProPhePheArgIysIyr 159
DB 1022 AGCTTCACGCGATCTACGAGTTCATGAGAACTTCCTTACTACCGCGAGAACAG 1081
QY 160 ThrGlyTTPArgAsnSerValArgHisIeuleuSerIeuleuAsnAspCysPheValIysVal 179
DB 1082 CAGGCTGCGAGAGACTCCATCCGCGACACCACTGCTCCCAAGGCTTCGGAAGGTA 1141
QY 180 LeuArgAspProSerArgProIyrIyrAspAsnIyrIyrMetIeuleuAsnProAsnSer 199
DB 1142 CCGCGCACTACGAGACCGCG-----GCGAGGCGACACTGATGATGCGAGCGGTGAGC 1198
QY 200 GluIyrThrPheAlaAspGlyVal-----PheArgArgArgIysArgIeuleuSer 216
DB 1199 GACGAGCTGTTATCGCGGCGACGACCGGCAAGCTGCGCGCGCTC-CACCACTCTCG 1257
QY 217 HisArgAlaProValProAlaProGlyIeuleuArgProGlnAlaProGlyIeuleuProAla 226
DB 1258 GGCACAGCTAGCTTAAAGCGCGCGCG-----ACG 1287
QY 237 AlaProProProAlaProAlaIaIaProAlaSerProArgMetArgSerProAlaArgGln 256
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QY 257 GluGluArgAlaSerProAlaGlyIysPheSerSerPheAlaIleAspSerIleu 276
DB 1329 ---CCCTTACTGCGCCATGT----- 1346
QY 277 ArgIysProPheArgSerArgIeuleuArgAspThrAlaProGlyIyrThrIeuleuIyr 296
DB 1347 -----CGCGCTTCTGCTCCGACACCACTGCGCGCA 1379
QY 297 GlyAla-----AlaProCysProProIeuleuProAlaPheProAlaIeuleu 311
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QY 312 ProAlaIaProCys-----ArgAlaIeuleuProIeu----- 322
DB 1434 CTTACAGCTCGGTTGACTCAAACTCGCTGGGCAACAACTCTTCTTCCACCGCGCA 1493
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QY 336 ArgGlnIaIeuleuValProProThrAlaProProIeuleuIeuleuAlaProIeuleuAla 355
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QY 375 uArgIeuleuProAlaIeuleu-----GlnAlaIeuleuValArgArgProGlyIyr 391
DB 1674 ACGT-----CCGCAACCCGTAATGACTTGCAGACGACGACGCTCAAGAGCGCGCGCG 1730
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DB 1731 CGTCTCTCTTAC 1743

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RESULT 11
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; Sequence 1, Application US/08331644
; Patent No. 5976872
; GENERAL INFORMATION:
; APPLICANT: Tao, Wufan

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? APPLICANT: Lai, Tseng
? TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
? TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF
? NUMBER OF SEQUENCES: 4
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Cooper & Dunham
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/331,644
? FILING DATE:
? CLASSIFICATION: 435
? PRIORITY INFORMATION:
? APPLICATION NUMBER: US 07/892,292
? FILING DATE: 13-MAY-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? REFERENCE/DOCKET NUMBER: 41472-A-PCT-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-278-0400
? TELEFAX: 212-391-0525
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2830 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEICAL: N
? ANTI-SENSE: N
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 443..1882
? OTHER INFORMATION:
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 926..1255
? OTHER INFORMATION: /note= "nucleotide sequence
? OTHER INFORMATION: encoding DNA binding domain
? OTHER INFORMATION: homology"
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? NAME/KEY: misc_signal
? LOCATION: 1883..1885
? OTHER INFORMATION: /note= "translation termination
? OTHER INFORMATION: codon"
US-08-331-644-1
US-10-087-080-32 (1-402) x US-08-331-644-1 (1-2830)
Alignment Scores:
Pred. No.: 5.32e-13 Length: 2830
Score: 400.50 Matches: 143
Percent Similarity: 40.47% Conservative: 29
Best Local Similarity: 33.65% Mismatches: 146
Query Match: 18.86% Indels: 109
Gaps: 18
OY 8 ProAarglaAlahlglyAsplysgIngIseraspLeugluGlyAlgLyGlySerasp 27
Db 683 CCCCCGAGCGGGCGGCACGCCCCAGCAGCGAGCAGCAGCACGACMAAGGC-----72
OY 28 AlaProSerProleu-----SerAlaAlaGlyAsp-----AspSer 39
Db 728 ---CCCGAGCGGTTCGTCCCGCCGTCGCGCCGCTCGCGCCGCTTGGAAGGGGGCCCAAGCGTGCACGCA 784

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Db	1022	ACGCTCAAGGGATCTACAGATTCACTCAAGAACTTCCTTACTACCGCAAGAACAG	108
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Db	1434	CCTTACAGCTCGGTGTGACTCAAACTCGTGGGCAACAACTCTTCTCCACGCA	1493
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RESULT 13  
US-08-331-644-4  
; Sequence 4, Application US/08331644  
; Patent No. 5976872  
; GENERAL INFORMATION:  
; APPLICANT: Tao, Wufan  
; APPLICANT: Lai, Bseung  
; TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/331,644  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/882,292  
; FILING DATE: 13-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41472-A-PCT-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1155 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-331-644-4

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Db 267 GACCGGCGCTCGGACACAGCATGACGCGC-----TTACTCGATTCGAGACC 317  
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QY 84 AlaValAlaAlaGluGlyAlaGluAlaAlaGlyProGlyAlaGlyGlyAla----- 102  
Db 378 CTAC-----GGCGCATGCGCGCGCGCGCGCGCTACTCGCGCGCGCGAGCA 428  
QY 103 ---GlySerGlyGlyGlyAlaArgSerLysProTyrThrArgArgPro----- 117  
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QY 118 -----LysProProTyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSe 134  
Db 489 GACCTGTGTAAGCGCGCTTACAGCTATATAGCGCTCATCATCAGCGCGCGCGAG 548  
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QY 174 pCysPheValLysValLeuArgAspProSerArgProTyrGlyLysAspAsnTyrTrpMe 194  
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QY 245 --ProAlaSerProArgMetArgSerProAlaArgGlnGlu-----A 259  
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QY 299 lAProCysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAla 319  
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RESULT 14  
PCT-US93-04102-4  
; Sequence 4, Application PC/TUS9304102





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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 2, 2004, 16:34:39 ; Search time 598 seconds

(without alignments)  
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Title: US-10-087-080-32

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Searched: 3267054 seqs, 2485319735 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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## Database:

Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2123	100.0	1209	13	US-10-229-345-9	Sequence 9, Appl1
2	2123	100.0	1209	16	US-10-274-171-9	Sequence 31, Appl1
3	2123	100.0	1209	16	US-10-087-080-31	Sequence 25, Appl1
4	2123	100.0	1209	17	US-10-650-112-9	Sequence 26, Appl1
5	2081.5	98.0	1212	17	US-10-650-112-25	Sequence 27, Appl1
6	1597	75.2	1203	17	US-10-650-112-26	Sequence 1814, Ap
7	1534	72.3	1203	17	US-10-650-112-27	Sequence 231533,
8	1412.5	66.5	1760	12	US-10-152-319A-1814	Sequence 231533,
9	716	33.7	585	16	US-10-027-632-231353	Sequence 1045, Ap
10	716	33.7	585	16	US-10-027-632-231353	Sequence 1045, Ap
11	488.5	23.0	2487	13	US-10-342-887-1045	Sequence 135, App
12	488.5	23.0	2487	13	US-10-172-118-1045	Sequence 802, App
13	488.5	23.0	2487	13	US-10-205-882-135	Sequence 1266, Ap
14	488.5	23.0	5181	12	US-09-969-807A-802	Sequence 947, App
15	487.5	23.0	2271	15	US-10-101-510-133	Sequence 611, App
16	470	22.1	320	9	US-09-833-881-1266	Sequence 1, Appl1
17	466.5	22.0	2187	10	US-09-960-706-947	Sequence 115, App
18	425	20.0	1662	13	US-10-342-887-611	Sequence 1132, App
19	425	20.0	1662	13	US-10-172-118-611	Sequence 1132, Ap
20	423	19.9	1662	10	US-09-292-862-1	Sequence 24, Appl
21	419.5	19.8	2753	15	US-10-007-280A-115	Sequence 10858, A
22	411	19.4	2559	13	US-10-342-887-1132	Sequence 24788, A
23	411	19.4	2559	13	US-10-172-118-1132	Sequence 18, Appl
24	411	19.4	3098	15	US-10-293-582-24	Sequence 455, App
25	411	19.4	3098	15	US-10-198-846-10858	Sequence 1049, Ap
26	407.5	19.2	1137	15	US-10-029-386-24788	Sequence 1049, Ap
27	407	19.2	5001	17	US-10-303-635-18	Sequence 211, App
28	406	19.1	2872	13	US-09-969-708-455	Sequence 8, Appl1
29	406	19.1	2872	13	US-10-342-887-1049	Sequence 1, Appl1
30	406	19.1	2872	13	US-10-172-118-1049	Sequence 1, Appl1
31	406	19.1	2872	13	US-10-388-360-310	Sequence 6, Appl1
32	406	19.1	2872	15	US-10-177-293-211	Sequence 94, Appl
33	405	19.1	3289	17	US-09-963-285-8	Sequence 95, Appl
34	405	19.1	3289	17	US-10-806-782-1	Sequence 9, Appl1
35	405	19.1	6458	9	US-09-963-285-6	Sequence 4, Appl1
36	403	19.0	2712	9	US-09-963-285-6	Sequence 496, App
37	403	19.0	2712	17	US-10-303-635-94	Sequence 497, App
38	403	19.0	6021	17	US-09-963-285-5	Sequence 497, App
39	403	19.0	6021	17	US-10-303-635-95	
40	391.5	18.4	1506	9	US-09-963-285-9	
41	391.5	18.4	1506	17	US-10-303-635-4	
42	391	18.4	4454	9	US-09-764-887-496	
43	391	18.4	4454	15	US-10-073-961-496	
44	387	18.2	4450	9	US-09-764-887-497	
45	387	18.2	4450	15	US-10-073-961-497	

## ALIGNMENTS

RESULT 1  
US-10-229-345-9  
; Sequence 9, Application US/10229345  
; Publication No. US20040038220A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKOWITZ, Sanford D.  
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS  
; FILE REFERENCE: CMRU-P01-003  
; CURRENT APPLICATION NUMBER: US/10/229, 345  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 1209  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1161) - (1161)  
; OTHER INFORMATION: n=a, c, g, or t  
US-10-229-345-9

Alignment Scores:

Pred. No.: 4,77e-153 Length: 1209  
 Score: 2123.00 Matches: 402  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-10-087-080-32 (1-402) x US-10-229-345-9 (1-1209)

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Qy      1 MetLysLeuGIuValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20
Db      1 ATGAAGTTGGAGGAGTTCCTCCCTCGCGCGGCCACCGGGGCAAGAGCGGGGAGACTG 60
Qy      21 GluGlyAlaGlyGlySerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db      61 GAGGCGCGGGCGGAGGAGCGCGCGCGCTCCGCTGTGCGGGGAGGAGACTCCCTG 120
Qy      41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyAlaArgAspThrGln 60
Db      121 GGCTCAAGTGGGACTGGCGCGGCCAAGCCGTCGCGCGCGCGCGCCAGAGATACGAG 180
Qy      61 GlyAspGlyGlnGlnSerAlaGlyGlyProGlyAlaGlnGluAlaIleProAlaAla 80
Db      181 GGCGACGGCGAAGAGTGGCGGAGCGCGCGCGCGGAGGAGCGCATCCCGCGAGCA 240
Qy      81 AlaAlaAlaAlaValAlaAlaGluGlyAlaGluAlaGlyAlaAlaIleProGlyAlaGly 100
Db      241 GCTCTGACGGCGGTGGTGGCGAAGGCGCGGAGCGGGGCGGGGCGCGAGCGCGGC 300
Qy      101 GlyAlaGlySerGlyGlnGlyAlaArgSerLysProTyrThrArgProLysProPro 120
Db      301 GGGCGGGGAGCGCGGAGGGTGGACGCGAGCAAGCATATACGGCGCGGCCAACGCCCCC 360
Qy      121 TyrseryTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThr 140
Db      361 TACTCGTACATCGCGCTCATCGCATGCGCATGCGCGAGCTGGGGGGCGCGCTTGACG 420
Qy      141 LeuAlaGluIleAsnGluTyrLeuMetGlyLysPheProPhePheArgLysSerTyrThr 160
Db      421 CTGGCGGAGATCAACAGATACCTCATGGGCAGATTCCCTTTTTCGGCGGAGCTACACG 480
Qy      161 GlyTyrParGAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValIysValLeu 180
Db      481 GGCTGGGCGCAACTCGGTGCGCGCACACACTTTCGCTCAACGACTGTTGTCAGGTGCTG 540
Qy      181 ArgAspProSerArgProTyrProlGlyLysAspAsnTyrTyrMetLeuAsnProAsnSerGlu 200
Db      541 CGCGACCCCTCGCGCGCTCGGGGCAAGCAACTATCTGATGCTCAACCCCAACAGCGGAG 600
Qy      201 TyrThrPheAlaAspGlyValPheArgArgArgArgLysArgLeuSerHisArgAlaPro 220
Db      601 TACACCTTTCGCGAGGGGATCTTCGCGCGCGCGCGCAAGCGCTGAGCACCGCGCGCG 660
Qy      221 ValProAlaProGlyLysLeuArgProGluGluAlaProGlyLysLeuProAlaAlaProProPro 240
Db      661 GTCCCGCGCGCGCGCGCTCGCGCGAGAGGCGCGCGCGCTCCCGCGCGCGCGCGCGCC 720
Qy      241 AlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluArgAla 260
Db      721 GCGCGCGCGCGCGCGCTCGCGCGCATGCGCTCGCGCGCGCGCAAGAGAGCGCGCC 780
Qy      261 SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuAlaLysProPhe 280
Db      781 AGCCCCGGGGAGATTCTCCAGCTCTTCGCGCATGACAGATCTCTCGCAGCCCTTC 840
Qy      281 ArgSerArgLeuArgAspThrAlaProGlyThrThrLeuGlnTyrGlyAlaAlaPro 300
Db      841 CGGAGCGCTCGCTCAGGAGACAGCGCGCGCGGAGAGAGCGTTCACTGGGGCGCGCGCC 900
Qy      301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
Db      901 TGCGCGCGCTGCGCGCGCTCCCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
  
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Qy      321 ProLeuCysAlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGluAlaGluVal 340
Db      961 CCGCTTGCGCGTACGGCGCGCGGAGACCGCGCGGCTGGCGCGCGCGCGAGCGGTG 1020
Qy      341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360
Db      1021 CCACCGACCGCGCGCGCTCTGCTGTGACCTCTCCCGGGGCGCGCGCGCGCGCGCAACCA 1080
Qy      361 LeuAlaGlyProAlaAlaGlyAlaAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380
Db      1081 CTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Qy      381 LeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSerTyrProValGluThrLeu 400
Db      1141 CTGAGGCGCGCTTACGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Qy      401 LeuAla 402
Db      1201 CTAGCT 1206
  
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RESULT 2  
 US-10-274-177-9  
 ; Sequence 9, Application US/10274177  
 ; Publication No. US20040038225A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MARKOWITZ, Sanford D.  
 ; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS  
 ; FILE REFERENCE: CRRU-P01-003  
 ; CURRENT APPLICATION NUMBER: US/10/274,177  
 ; PRIORITY FILING DATE: 2002-10-18  
 ; PRIOR APPLICATION NUMBER: US/10/229,345  
 ; PRIORITY FILING DATE: 2002-08-26  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 1209  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1161)..(1161)  
 ; OTHER INFORMATION: n=a, c, g, or t  
 US-10-274-177-9

Alignment Scores:  
 Pred. No.: 4,77e-153 Length: 1209  
 Score: 2123.00 Matches: 402  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-10-087-080-32 (1-402) x US-10-274-177-9 (1-1209)

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Qy      1 MetLysLeuGIuValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20
Db      1 ATGAAGTTGGAGGAGTTCCTCCCTCGCGCGGCCACCGGGGCAAGAGCGGGGAGACTG 60
Qy      21 GluGlyAlaGlyGlySerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db      61 GAGGCGCGGGCGGAGGAGCGCGCGCGCTCCGCTGTGCGGGGAGGAGACTCCCTG 120
Qy      41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyAlaArgAspThrGln 60
Db      121 GGCTCAAGTGGGACTGGCGCGGCCAAGCCGTCGCGCGCGCGCGCCAGAGATACGAG 180
Qy      61 GlyAspGlyGlnGlnSerAlaGlyGlyProGlyAlaGlnGluAlaIleProAlaAla 80
Db      181 GGCGACGGCGAAGAGTGGCGGAGCGCGCGCGCGGAGGAGCGCATCCCGCGAGCA 240
Qy      81 AlaAlaAlaAlaValAlaAlaGluGlyAlaGluAlaGlyAlaAlaIleProGlyAlaGly 100
Db      241 GCTCTGACGGCGGTGGTGGCGAAGGCGCGGAGCGGGGCGGGGCGCGAGCGCGGC 300
  
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QY	101	GIYALAGLYSERGIYGLNLIYALAAAGSERIYSPROYTHIRARARPROCIYSPROB	120
Db	301	GGCGGGGAGACGGCGAGGATGACGCAACAGCCATATACGGGGGGCCCAAGCCCCC	360
QY	121	TYRSEYIILEALALEUILAELAMELAIILEARGASPERALAGLYARGLEUTHR	140
Db	361	TACTGTAACATCGCGCTCATGCGCATGCGCATCCCGGACTCGGGCGGGCGCTTGAGC	420
QY	141	LEUALAGLITLEASGLITRYILEUWETGLYISPHIEPROPHENHARGLYSEYTRYTHR	160
Db	421	CTGGGGGAGATCAAGAGTAACATGAGGCAAGTCCCTTTTTCGGCGGAGCTAACAG	480
QY	161	GIYTPRARGASNSERVAIARHISANSLEUSERTLEUASASPQYSPHEHALYSTALLEU	180
Db	481	GGCTGAGCGAAGCTCGGTGCGCAACACTTGCTTCACAGACTGCTTCCTCAAGGTGCG	540
QY	181	ARGASPPROSERARGPROTRIPGLIYASAPASNTYTRYMETLEUASNTROASNSERGIN	200
Db	541	CGCGACCCCTCGCGGGCCCTGGGGGCAAGGACAATCTGATCTCAACCCCAACAGCGAG	600
QY	201	TYRTHRPHENIILASGLIYALPHEARGARGARGLYSARGLEUSERHISARGALAPRO	220
Db	601	TACACCTTTCGCGAGGGGGTCTTCGCGCGCCCGCAAGCGCTCAAGCCACCGCGCGCG	660
QY	221	VALPROIALPROGLIYLEUARGPROGLIUNIALIAPROGLIYLEUPROIALAPROBPRO	240
Db	661	GTCCCCGGCCCCGGGGCTGGGGCCCAAGAGGCCCGGGCTTCCCGCGCCCCCGCGGCC	720
QY	241	ALAProIALIAPROIALASERPROARGMETARGSERPROIALIARGIINGIUNARGIALA	260
Db	721	GGGCGCGCGCCCGCGCTCGCGCCCGCAGTGCCTGCGCGCCGCGCAAGAGAGGGCGGC	780
QY	261	SERPROIAGLYLYSPHESERSESERPHEALILEASPERILLEUARGLYSPROPHE	280
Db	781	AGCCCCGGGGGAGATTTCTCCAGCTCTTGCCATCGACAGCATCTGTGGCAAGCCCTTTC	840
QY	281	ARGSERARGARGLEUARGASPTHRIAPROGLIYTHRIEUNGINTRPGIYALIAIAPRO	300
Db	841	CGACACCTCGCTGACGAGGACACGGCCCCCGGAGACAGACCTTCAATGGGGCGCGCGGCC	900
QY	301	CYSPROPROLEUPROIALPHEPROIALALEUENUPROIALIAPROCYSAHIALALEUEN	320
Db	901	TGCCCGCGCGTCCCGCGCTCCCGCGCTCTCCCGCGCGCGCTTGACAGGGCCCTGCTG	960
QY	321	PROLEUCYSALITYRGLYVALAGLYLUPROIALAAGLEUNGIALIARGIUNIAAGIUNIAI	340
Db	961	CGGCTCTCGGGTACGGCGGGCGAGCGGGCGGGCTGGGGCGCGGAGGCGCAAGGTG	1020
QY	341	PROPROTHRIAPROPROLEUENLEUENALAPROLEUPROIALIAPROIALAPRO	360
Db	1021	CCACCGGACGGCGCGCCCTCTCTGCTTGACCTCTCCGGGGCGGGCCCCCGCAAGCCA	1080
QY	361	LEUARGLYPROIALIAGLYGIALIHSIENURYCYSPROLEUARGLEUPROIALIAA	380
Db	1081	CTCCGAGGCGCGCGCGCGCGCGCACCTGTACTGCCCTCGGCTGGCGCGACGCG	1140
QY	381	LEUNGIALIALAENVALARGARGPROGLIYPROHISLEUSERTRYPROVALGINTHRIEN	400
Db	1141	CTGACGGGGGCGCTTATGTCGACGCTCTGACCGCGCACCTGTGTACTCCGATGAGACGCTC	1200
QY	401	LEUALA 402	
Db	1201	CTAGCT 1206	

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: APPLICANT: Case Western Reserve University
: TITLE OF INVENTION: No. US20030235820A1el Methods of Diagnosis of Metastatic Colore
: TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
: TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
: FILE REFERENCE: 018501-0008400S
: CURRENT APPLICATION NUMBER: US/10/087,080
: PRIOR FILING DATE: 2002-10-25
: PRIOR APPLICATION NUMBER: US 60/272,206
: PRIOR FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: US 60/281,149
: PRIOR FILING DATE: 2001-04-02
: PRIOR APPLICATION NUMBER: US 60/284,555
: PRIOR FILING DATE: 2001-04-17
: NUMBER OF SEQ ID NOS: 41
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 31
: LENGTH: 1209
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: winged helix/boxhead transcription factor (HIFI1)
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: (1161)
: OTHER INFORMATION: n = g, a, c or t
: US-10-087-080-31

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Alignment Scores:

Pred. No.:	4,77e-153	Length:	1209
Score:	2123.00	Matches:	402
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

US-10-087-080-32 (1-402) X US-10-087-080-31 (1-1209)

QY	1	MeLysLeuGIuValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu	20
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QY	21	GIuGIyValGIyGIySerAspAlaProSerProIeuSerAlaAlaGlyAspAspSerIeu	40
Db	61	GAGGGGGCGGGGGCGAGCACCGCGCGTCCCGCTGTCTGGCGGGGAGACGACTCCCTG	120
QY	41	GlySerAspGIyAspCysAlaAlaIalysProSerAlaGlyGlyAlaAlaArgAspThrGln	60
Db	121	GGCTCAGATGGGGACTGGCGGCCAGACCGTTCGGCGGGCGCGCGGCCCAAGATACGAG	180
QY	61	GlyAspGIyGIuGlnSerAlaGlyGlyGlyProGlyAlaGluGluAlaIleProAlaAla	80
Db	181	GGCGACGGGGAACAGCATGCGGGAGGCGGGCGGGCGGGAGGAGCATCCGGCGAGCA	240
QY	81	AlaAlaAlaAlaValValAlaGlnGlyAlaGluAlaGlyAlaAlaGlyProGlyValaGly	100
Db	241	GCTCTCCAGCGGTGTGGCGAGGGCCCGGAGGCGGGGGCGCGAGGGCGGGCG	300
QY	101	GIyAlaGlySerGIyGIuGlyAlaArgSerLysProTyrThrArgArgProLysProPro	120
Db	301	GGCGCGGGAGCGCGAGGGGTGCACGACGACAGCCATATACGGCGGGCCCAAGCCCCC	360
QY	121	TyrSerTyrIleAlaIleuIleAlaIleuAlaIleArgAspSerAlaGlyGlyAlaGluThr	140
Db	361	TACTCGTACATGCGCTCATCGCCAGGCGACATCGGACATCGGGGGCGGGCGGTGACG	420
QY	141	IleuAlaGluIleAsnGluTyrLeuMetGlyLysPheProPheArgGlySerTyrThr	160
Db	421	CTGGCGGAGATCAAGAGTACCTCATGGGCAAGTTCCCTTTCCGGGGAGGTACAG	480
QY	161	GlyTyrArgAsnSerValArgHisAsnIeuSerIeuAsnAspCysPheValIleValLeu	180
Db	481	GGCTGGCGCACTCCGTGGCGCAACCTTTCGCTCAACAGATGCTTCGTCAAGAGTCTG	540

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QY 181 ArgAspProSerArgProTpgLyAspAsnTyrTrpMetLeuAsnProAsnSerGlu 200
Db 541 CGGACCCCTCGGGCCCTGAGGCAACCACTTCTGATGCTCAACCCCAAGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgGlySerLeuSerHisArgAlaPro 220
Db 601 TACACCTGCGCGAGCGGGGTCTTCCGCGCGCGCAAGCGCTCAGACCAACCGCGCGCG 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 241 AlProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluArgAla 260
Db 721 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTpgLyAlaAlaPro 300
Db 841 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 301 CysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArgAlaLeuLeu 320
Db 901 TGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 321 ProLeuCysAlaTyrGlyAlaGlyGluProAlaArgLeuGlyAlaArgGluAlaGlyVal 340
Db 961 CCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 341 ProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAlaAlaProAlaLysPro 360
Db 1021 CCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
QY 361 LeuArgGlyProAlaAlaGlyGlyAlaHisLeuTyrCysProLeuArgLeuProAlaAla 380
Db 1081 CTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 381 LeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSerTyrProValGluThrLeu 400
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QY 401 LeuAla 402
Db 1201 CTAGCT 1206

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## RESULT 4

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US-10-650-112-9
; Sequence 9, Application US/10650112
; Publication No. US20040110712A1
; GENERAL INFORMATION:
; APPLICANT: MARROWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CMRU-F01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1161)..(1161)

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OTHER INFORMATION: n is a,t,g or c  
US-10-650-112-9

Alignment Scores:  
Pred. No.: 4,77e-153  
Score: 2123.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 17  
Matches: 1209  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-10-087-080-32 (1-402) x US-10-650-112-9 (1-1209)

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QY 1 MetLysLeuGluValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20
Db 1 ATGAAAGTTGAGGAGTGTTCCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
QY 21 GlnGlyAlaGlyLysSerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
Db 61 GAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 GlySerAspGlyAspCysAlaAlaLysProSerAlaGlyGlyLysAlaArgAspThrGln 60
Db 121 GGCTCAGATGGGACATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 GlyAspGlyGlnGlnSerAlaGlyGlyProGlyValaGlnGluAlaIleProAlaAla 80
Db 181 GCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 AlAlaAlaAlaValAlaAlaGlnGlyValaGlnAlaGlyAlaAlaGlyProGlyValaGly 100
Db 241 GCTGTCGACGCGGTGTGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 101 GlyAlaGlySerGlyGlnGlyAlaArgSerLysProTyrThrArgArgProLysProPro 120
Db 301 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 TyrSerTyrIleAlaLeuIleAlaMetAlaIleArgAspSerAlaGlyGlyArgLeuThr 140
Db 361 TACTCGACATCCGCGTCATCGCATGCGCATCGGACCTCGGCGCGCGCGCGCGCGCG 420
QY 141 LeuAlaGluIleAsnGlnTyrLeuMetGlyLysPheProPheArgGlySerTyrThr 160
Db 421 CTGCGGAGATCAACGAGTACTCATGGGCAAGTCCCTTTTCCCGGAGCTTACACG 480
QY 161 GlyTyrArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysValLeu 180
Db 481 GGCTGGCGCAACTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 181 ArgAspProSerArgProTpgLyLysAspAsnTyrTrpMetLeuAsnProAsnSerGlu 200
Db 541 CGGACCCCTCGGGCCCTGAGGCAACCACTTCTGATGCTCAACCCCAAGAG 600
QY 201 TyrThrPheAlaAspGlyValPheArgArgArgGlySerLeuSerHisArgAlaPro 220
Db 601 TACACCTGCGCGAGCGGGGTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 221 ValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAlaAlaProProPro 240
Db 661 GTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 241 AlProAlaAlaProAlaSerProArgMetArgSerProAlaArgGlnGluArgAla 260
Db 721 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 261 SerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIleLeuArgLysProPhe 280
Db 781 AGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 281 ArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTpgLyAlaAlaPro 300
Db 841 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900

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; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CMRU-P01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: MOUSE FOXQ1
; US-10-650-112-26

Alignment Scores:
Pred. No.: 5.63e-113 Length: 1203
Score: 1597.00 Matches: 320
Percent Similarity: 82.27% Conservative: 14
Best Local Similarity: 78.82% Mismatches: 62
Query Match: 75.22% Indels: 10
DB: 17 Gaps: 6

US-10-087-080-32 (1-402) x US-10-650-112-26 (1-1203)
QY 1 MetLysLeuGluValPheValProArgAlaAlaHisGlyAspLysGlnGlySerAspLeu 20
DB 1 ATAAATTTGAGAGTGTTCCTCCACGGGACGCCCGGAGCAAAATGGGACGATCTG 60
QY 21 GlnGlyAlaGlyLysSerAspAlaProSerProLeuSerAlaAlaGlyAspAspSerLeu 40
DB 61 GAGGGGGCGCGGACGAGCGAGCTGCATCTCCACTGTCCGGCTGGTACGACTCTTA 120
QY 41 GlySerAspGlyAspCysAlaAla---LysProSerAlaGlyLysAlaAlaGlyAspThr 59
DB 121 GGCTCAGACGGGACTGTGACGCAACAGCCCGCGGGCGGACGGCGGCGGATCTG 180
QY 60 Gln---GlyAspGlyGlnSerAlaGlyGlyProGlyAlaGlnAlaAlaPro 78
DB 181 GAGAGTGGCGCGCGGAGAGAAATCGAGTGGCGCGCGGACGCCCAAGCGGTCCGAG 240
QY 79 AlaAlaAlaAlaAlaAlaValAlaGlnGlyAlaGlnAlaGlyProGly 98
DB 241 GCAACTGATGACAGACA-----ACGCAAGCTCTCCGGCGAGGGCGGTGC 285
QY 99 AlaGlyGlyAlaGlySerGlyGlnGlyAlaArgSerLysProThrArgArgProLys 118
DB 286 GCGGGCGCGGTGGCGCGGCGGAGGGCGCGGACGAGCGGTAACGCGCGGCCCAAG 345
QY 119 ProProLysSerLysLysAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 138
DB 346 CCCCCAATCTCCATCATCGCTCATGTGCATGCCATCCGCACTCCGGCGGAGCGC 405
QY 139 LeuThrLeuAlaGlnLeuGlnGlyLysLeuMetGlyLysPheProPheArgGlySer 158
DB 406 CTGACACTGGCCGAGATCAAGATCACTCATGGGCAAGTTCCCTTTTCCGGGCGAGC 465
QY 159 TyrThrGlyThrArgAnserValArgHisAsnLeuSerLeuAnserCysPheValLys 178
DB 466 TACACGGGCTGGGCAACTCCGTGCGCAACCTCTCGCTCAACGACTTTTCGTCAAG 525
QY 179 ValLeuArgAspProSerArgProTrpGlyLysAspAsnTyrTrpMetLeuAsnProAsn 198
DB 526 GTGTGTGGCAACCCCTCGCGGCGCTGGGGCAAGACAACACTACTGATGCTCAACCCCAAC 565
QY 199 SerGlnTyrThrPheAlaAspGlyValPheArgArgArgArgLysLeuSerHisArg 218
DB 586 AGCGAATACACTTTCGCGGAGGGGCTTTCGCGCGCGGCAAGCGCTCAGCACCGG 645

```

```

QY 219 AlaProValProAlaProGlyLeuArgProGlnGlnAlaProGlyLeuProAla---Ala 237
DB 646 ACCACAGTCTCGCGCGCGGCTGCGGAGAGAAAGCCCAACCGGACTCTCCGGAGAC 705
QY 238 ProProProAlaProAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 257
DB 706 CCGCAGCCCGCGCGCGCGCGCGCTTCGCCGATCGCGCGCTCGCGCGCTCGCCAGAG 765
QY 258 GlnArgAlaSerProAlaGlyLysPheSerSerSerPheAlaAlaAspSerLeuLysArg 277
DB 766 GAGCGCTCCAGCGCGCGGAGCAAGTCTCCACTCTTCGATGACGACGACTTCACG 825
QY 278 LysProPheArgSerArgArgLeuArgAspThrAlaProGlyThrThrLeuGlnTrpGly 297
DB 826 AAGCTTTTCGACAGCGCGCGGACGCGGACGCTGCTGGGCGTGAAGTACCTCGGG 885
QY 298 AlaAlaProCysProProLeuProAlaPheProAlaLeuLeuProAlaAlaProCysArg 317
DB 886 GCGGCTCCTGCGCGCGCGCTGCGCGCTATCCCGGCTCTTCGCGCGCGCGGTGGC 945
QY 318 AlaLeuLeuProLeuCysAlaTyrGlyAlaGlyGlnProAlaArgLeuGlyAlaArgGln 337
DB 946 GCTCTGCTACCGCTCTGTGCTTACGCGGACGAGCTTACGCTGCTGGCGTGGCGG 1005
QY 338 AlaGluValProProThrAlaProProLeuLeuAlaProLeuProAlaAlaAlaPro 357
DB 1006 ACCGAGGTGACGCGCGCGG---CCCTCTGTCTGCGCGCTCTCCACCGGCGTCCA 1062
QY 358 AlaLysProLeuArgLysPro---AlaAlaGlyAlaHisLeuTyrCysProLeuArg 376
DB 1063 GCCAAGCCCATTCGAGAGTCCGAGACCGCGCGGCGGCGCACCTGATGATGCCCCCTAC 1122
QY 377 LeuProAlaAlaLeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSerLysPro 396
DB 1123 CTGCCACGCGCGCTGCGAGCGGCGAGCGGCTGGTCCGATCCGATCCTGCTACCG 1182
QY 397 ValGlnThrLeuLeuAla 402
DB 1183 GTGGAGACTCTGTGACT 1200

RESULT 7
US-10-650-112-27
; Sequence 27, Application US/10650112
; Publication No. US20040110712A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
; FILE REFERENCE: CMRU-P01-044
; CURRENT APPLICATION NUMBER: US/10/650,112
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/274,177
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/229,245
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/406,296
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: RAT FOXQ1
; US-10-650-112-27

Alignment Scores:
Pred. No.: 3.55e-108 Length: 1203
Score: 1534.00 Matches: 311
Percent Similarity: 79.90% Conservative: 15
Best Local Similarity: 76.23% Mismatches: 68
Query Match: 72.26% Indels: 14
DB: 17 Gaps: 7

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US-10-087-080-32 (1-402) x US-10-650-112-27 (1-1203)

QY 1 MetLysLeuGluValPheValProAlaGlaAlaHisGlyAspLysGlnIleSerAspLeu 20  
Db 1 ATGAATAATTGAGGTATTGCCCCACCGCAGCCCAAGGGGACAAAGTGGCAGTACCTCG 60  
QY 21 GluGluValAlaGlySerAspAlaProSerProLeuSerAlaAlaIleAspSerLeu 40  
Db 61 GAGGGGGCCGCGACGACGACGTCATCTCCGCTGCGCGGCTGGCAGCACTCTTA 120  
QY 41 GlySerAspGlyAspCysAlaAla---LysProSerAlaGlyGlyValAlaArgSpThr 59  
Db 121 GCTCTGACGGGAGACTGTGACGCCAACCGCCGCGCGGAGAGAGCCCTGATCTG 180  
QY 60 Gln---GlyAspGlyGluGlnSerAlaGlyGlyProGlyAlaGluAlaIlePro 78  
Db 181 GAAGGGGGGGGGGCGAGAGAGATTGAGTGGCGGGGCGAGAGCCCAAC----- 231  
QY 79 AlaAlaAlaAlaAlaValAlaValAlaGluGlyAla-----GluAlaGlyAlaAlaGly 96  
Db 232 -----GATCCCGAGGTGACCGCATGGCAGAGAACGAGGCTCCCGGTGGG 279  
QY 97 ProGlyAlaGlyGlyAlaGlySerGlyGlyGlyAlaArgSerLysProThrArgArg 116  
Db 280 CCGTCCGGGGGCGAGGTGGCGCGGTGAGGGCGCGCGAGAGCCGTAACAAGCGCGG 339  
QY 117 ProLysProProLysSerTyrlleAlaLeuIleAlaMetAlaIleArgAspSerAlaGly 136  
Db 340 CCCAAGCCCCCTACTCTCATTCGACCTCATCGCATGGCCATCCGCACTCCCGGGG 399  
QY 137 GlyAlaGluThrLeuAlaGluIleAsnGlyLysMetGlyLysPheProPhePheArg 156  
Db 400 GGACCGCTGACCTGGCGCCGAGATCAACGAGTACCTATGGGCAAGTCCCTTTTCCG 459  
QY 157 GlySerTyrlleThrGlnSerValArgHisAsnLeuSerLeuAsnAspSerPhe 176  
Db 460 GGACGCTACAGGGGCTGGCGCACTCCGCGCCCAACCTCTGCTCAACACGTTTC 519  
QY 177 ValLysValLeuArgAspProSerArgProTfpgLysAspAsnTyrlleMetLeuAsn 196  
Db 520 GTCAAGTCTCGCGGACCCCTCGCGGCTGGGGCAGAGAAATTAAGTGGTCTCANC 579  
QY 197 ProAsnSerGlyTyrllePheAlaAspGlyValPheArgArgArgArgLysLeuSer 216  
Db 580 CCCAACAAGGATPACACCTTCGCCGACGGGGCTTCGCGCGCGCGAAGCGCTCAGC 639  
QY 217 HisArgAlaProValProAlaProGlyLeuArgProGluGluAlaProGlyLeuProAla 236  
Db 640 CACCGGACCAACGTCCTCGCATCGGGCTACGCGCGAGAGAGCCCAACCCGACCTTGG 699  
QY 237 ---AlaProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArg 255  
Db 700 GGGACCCCGCAGACCCGCGCCACCGCGGCTCTCCCAATGGCGGCTCGCGCTGCG 759  
QY 256 GlnGluGluValAlaSerProAlaGlyLysPheSerSerSerPheAlaIleAspSerIle 275  
Db 760 CAGGAGGAGGGGCTCCAGCCCGCGAGCAAGTCTCCAGCTCTTGCCATCGACGATC 819  
QY 276 LeuArgLysProPheArgSerArgArgLeuArgArgPThrAlaProGlyThrThrLeuGln 295  
Db 820 CTCAGCAAGCCGTTTCGACGCGCGCAGCGGACCGCGCTCTGGGGTGGACCTACCC 879  
QY 296 TrpGlyAlaAlaProCysProProLeuProAlaPheProAlaLeuLeuProAlaAlaPro 315  
Db 880 TGGAGCGCTGCTCTGCGCGCGCGCTGCTTACCGCGCTCTTCCCGCGTCTGCC 939  
QY 316 CysArgAlaLeuLeuProLeuCysAlaArgLysAlaGlyGluProAlaArgGluGlyAla 335  
Db 940 GCGGGTGGCCCTGCTCGCTGCTGCTTACGCGCGGGGAGACCCACGCTGTGCGCTGC 999  
QY 336 ArgGluAlaGluValProProThrAlaProProLeuLeuLeuAlaProLeuProAlaAla 355  
Db 1000 GCGGGGGCGAGGTGACCGCGCGG---CCCTGTTGCTGGCGCCCTCTTCCACCGCG 1056

QY 356 AlaProAlaLysProLeuArgGlyPro---AlaAlaGlyGlyAlaHisLeuTyrlleCysPro 374  
Db 1057 GCGCCAGCGCAAGCATTTCGAGGTCCGAGACCGCGCGGCGCACCTGTACTGCCCC 1116  
QY 375 LeuArgLeuProAlaAlaLeuGlnAlaAlaLeuValArgArgProGlyProHisLeuSer 394  
Db 1117 CTACCGCTGCCACCGCCCTTCGAGGCGGCGCGCTGGCGGTCCGGGTCCGACCTGTCC 1176  
QY 395 TyrProValGluThrLeuLeuAla 402  
Db 1177 TACCGGTGGAGACGCTGCTAGCT 1200

RESULT 8  
US-10-152-319A-1814  
; Sequence 1814, Application US/10152319A  
; Publication No. US20040072160A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgs, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/10/152,319A  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/330,462  
; PRIOR FILING DATE: 2001-10-22  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2221  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1814  
; LENGTH: 1760  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. NM\_022858

US-10-152-319A-1814

Alignment Scores:  
Pred. No.: 9,12e-99 Length: 1760  
Score: 1412.50 Matches: 300  
Percent Similarity: 77.64% Conservative: 16  
Best Local Similarity: 73.71% Mismatches: 78  
Query Match: 66.53% Indels: 17  
DB: 12 Gaps: 6

US-10-087-080-32 (1-402) x US-10-152-319A-1814 (1-1760)

QY 1 MetLysLeuGluValPheValProAlaGlaAlaHisGlyAspLysGlnIleSerAspLeu 20  
Db 207 ATGAATAATTGAGGTATTGCTTCCACGCGCAGC-CACGGGGAACAAATGGGACGCACTCG 264

QY		21	GIHLGLVLAAGLYGlySerAspAlaProSerProLeuSerAlaIAGLVASPSerLeu	40
Db		265	GAGGGGGCCCGACAGCAGCTGCATCTCACGTCCGGGGCTGGACACTCTTA	324
QY		41	GLYSerASPGLyASPcysAlaA---LysProSerAlaIGLyGVAlaArgASpThr	59
Db		325	GGCTCAAGCCGGGGACTGTGCAGCCACAAGCCCCGGGGGAGGGGCCGGGGATCTG	384
QY		60	GLN---GLYasrGlyGIuGlInSerAlaGlyGlyGlyProGlyVlaGIuGlVallePro	78
Db		385	GAAGGTGGCCGGCCGAGAGGAATTTCAGTGGCCGGGGGAGACCACCCAGAC-----	435
QY		79	ALAalaAlaAlaAlaValValAlaGIuGlValA-----GIuAlaGlyVlaAlaGly	96
Db		436	-----GATCCCGAGGTGACCATGTGCAGCAGACAGCAGGCTCCCGGTGGG	483
QY		97	PROGLyAlaGlyGIyAlaGlySerGIuGlValAArgSerLysProTYrThrArgAr	116
Db		484	CCGTCGGGGCCACAGCTGGGGCGGGGTGAGGGCGCGCCACACAGCCGTACACGGCGGG	543
QY		117	ProlYsProPoyTySerTYrTlleAlaLeuIleAlaMetAlalleArgSPserAlaGly	136
Db		544	CCCAGAGCCCCCTCTCTTACATGCATCTCAGCATGCCATGCCATCCGAGCTCCGGCGAGC	603
QY		137	GLYArgLeuThrLeuAlaGluIleAsnGIuTYrLeuMetGIyLysPheProPhePhArg	156
Db		604	GGAGCGCTGCAGCTGGCCGAGAATCAACAGATCTCAAGGGACAAATTCCCTTTTCCGG	663
QY		157	GLYSerTYrThrGIyTYrTPArgASnservalArgHisLenLeuSerLeuAsnASPcysPhe	176
Db		664	GGCAGCTACAGGGGTGGCGCACCTCGTGCGCCACAACTCTGCTCAAGACTGTTTC	723
QY		177	VallYsValleuArgASPProSerArgProTrpGlyLysASPsrTYrTYrMetLeuasn	196
Db		724	GTCAAAGGTGTGGCGGACCCCTCGCGGCGCTGGGGCAGAGCAATTATCGATGCTCAAC	783
QY		197	ProHsnSerGIuTYrThrPheAlaSPGLyValPheAlaGArgArgLysArgLeuSer	216
Db		784	CCCAACAGCCGAATCACCTTGCGCGACGGGGCTTCGCCCGCGCGGCAAGCGCTTCAGGC	843
QY		217	HISArgAlaProValProAlaProGlyLeuArgProGIuGlValAProGlyVleuProAla	236
Db		844	CACCGGACCAACAGTCTCCGCATCGGGCTACGGCCGAGAGAACCCACCCGGACTCGGGGG	903
QY		237	AlaProProProAlaProAlaAlaABroAlaSerProArgMetLysSerProAlaArgIn	256
Db		904	ACCCCGCAGCCCGCGCCACCGCGGGCTCTCCCAATCGCGGCTCGCCGCGCCAG	963
QY		257	GIuGIuAlaGlaserProAlaGlyLysPheSerSerPheAlaIlleASPserTlleu	276
Db		964	GAGGAGGGCTCCAGGCCCGGACGACGAAGTTCACACTCTTCGCCATGACAGCATCTCTC	1022
QY		277	ArgLysProPheArgXSerArgArgLeuArgASPThrAlaProGlyThrThreusInTrp	296
Db		1024	AGCAAGCCGTTTCGACGCGCGGCA-CGGCACCCCGGCTTGGGGGTGCAGTACCCTGG	1082
QY		297	GLYAlaAlaProCYsProProLeuProAlaPheProAlaleuLeuProAlaAlaProCYs	316
Db		1083	AGCGGTGCTCCCTGGCCGCGCGGTGGCGGCTATCCGCGGCTCTCCGCGCGTCCGGAG	1144
QY		317	ArgAlaLeuLeuProLeuCysAlaTYrGlyValGlyGIuProAlaArgLeuGIyValArg	336
Db		1143	GGTGGCTCTGGCCGCTGTGTCTTACGGCGC-GGCGAGCCACACCTGTGGCTGGCGGC	1201
QY		337	GIuAlaGIuValAProProThraAlaProPheLeuLeuAlaProLeuProAlaAlaAla	356
Db		1202	GGGGCCGAGGTGCAGCCCGCGGG---CCCTGTTCGTGGGCCCCCTTCCACCGGGGCC	1255
QY		357	ProAlaLysProLeuArgGIyPro---AlaAlaGlyValAlansLeuTYrCySProLeu	375
Db		1259	CCAAGCAAGCCATTTCAGAGTCCGGAGAACCGCGCGCGGCSACCTGTACTGCCCTTA	1311
QY		376	ArgLeuProAlaAlaLeuGlAlaAlaLeuValA-ArgArgProGlyProHisLeuSerTYr	395

Dd		1319	CGGCTGCCACGGGCTTCAGCGCGCCGCGGCCTCGGCTCCTGGGTCCGCACTGTCTTAC	1378
Qy		396	ProValgluthrIleuLeuAla	402
Dd		1379	CGGGTGAGAGCGCTGTACT	1399
 RESULT 9 US-10-027-632-231353/c Sequence 23153, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION: APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide POLYMORPHISMS IN THE HUMAN GENOME FILE REFERENCE: 108827.129 CURRENT APPLICATION NUMBER: US/10/027.632 CURRENT FILING DATE: 2002-04-30 PRIORITY APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20 PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23 PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09 NUMBER OF SEQ ID NOS: 325720 SOFTWARE: FastSeq for Windows Version 4.0 SEQ ID NO 231353 LENGTH: 585 TYPE: DNA ORGANISM: Human US-10-027-632-231353				
 Alignment Scores:				
Pred. No.:	3,81e-46	Length:	585	
Score:	716.00	Matches:	136	
Percent Similarity:	97.84%	Conservative:	0	
Best Local Similarity:	97.84%	Mismatches:	3	
Query Match:	33.73%	Indels:	0	
DB:	13	Gaps:	0	
 US-10-087-080-32 (1-402) x US-10-027-632-231353 (1-585)				
Qy		264	GlyLysPheSerSerSerPheAlaIleAspSerIleuArgLysProPheArgSerArg	283
Dd		583	GGAAGAATCTCCAGCTCTCTCGCCATCGACAAGCATCTGCGCAACCCTTCGCGACGCCCG	524
Qy		284	ArgLeuArgaspThrAlaProGlyYthrThrIeuGlnTrpGlyAlaAlaProCysPropro	303
Dd		523	CGCCCGAGGAAACGCGCCCCCGGCGACGAGCTTCAGTGGGGCGCGCGCTGCGCCGCG	464
Qy		304	IeuProAlaIlePheProAlaIleuLeuProAlaAlaProCysArgAlaIleuLeuProLeuCys	323
Dd		463	CTGCCCGCGTTCCCGCGCTCTCTCCCGCGCGCCCTGAGGGCCCTGTGCGCGCTGCG	404
Qy		324	AlaTyrgLyAlaGlyGluProAlaArgIeuGlyAlaArgGlnAlaGlyValProProThr	343
Dd		403	GGGTACGGCGGGCGAGCGCGCGCGCTGGGGCGCGCGGRGCGAGGTGCCACCGAAC	344
Qy		344	AlaProProIleuLeuLeuAlaProIleuProAlaAlaAlaProAlaIlyProIleuArgGly	363
Dd		343	GGCGCGCGCTCTCTCTGCACTTCCCGGGGGGGCGCCCGCAAGCACTCCGAGGCG	284
Qy		364	ProAlaAlaGlyGlyAlaHisIleuTyrcysProLeuArgLysIeuProAlaAlaIeuGlnAla	383
Dd		283	CGGGGGCGCGGGCGGCGCACCTGTACTGCCCCCTGCGGCTGCCGCAAGCTTCGAGGGG	224





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Db      889 CCCCTACTACCGGAGAGATTCCCGCTGAGAGACATCCGCAACTCTCGCT 948
Qy      172 uaaaspCysPheValIysValLeuArgAspProSerArgProIrrpGlyysAspAnty 192
Db      949 CAAAGACTGCTTCTCAAGATCCCCCGAGACCCGGAACCGG--GCAAGGGCAACTA 1005
Qy      192 rTtMetLeuAsnProAsnSerGlyIrrPheAlaAspGlyValPheArgArgAr 212
Db      1006 CTGGACCTGGACCGGAGTCCCGGACATGTTGACACAGCGAGCTTCTCGGCGGAG 1065
Qy      212 glyAsrGleuSerHisArgAlaProValProAlaProGlyLeuArgProGluAla-- 231
Db      1066 GAAGCGCTTCAAG--CGGACGCGCTGCTCCACCCAGCGCGCGCGCGAGTCTCT 1122
Qy      232 -----ProGlyLeuProAlaAla----- 237
Db      1123 GCTGCTGCGGCGCGGAGCGGAGCGGCGGCGGAGCGGAGCGGCGCGCGCT 1182
Qy      238 ---ProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgI 256
Db      1183 CTTCGCCGCGCGC--GCCCGCGCGCGCGCGCATGCTAGGCTAGG--CGCTACGGCT 1238
Qy      256 ngIuGIuArgAlaSerProAlaGlyIysPheSerSerPheAlaIleAspSerIle 276
Db      1239 GCGGCTACGGCGCTGAGCTGCC-----GCCTTACGGCGCGCGCTCGACCTCTTCG 1289
Qy      276 uArgIysProPheArgSerArgArg-----LeuArgAspThrAlaPr 290
Db      1290 CCGCGGAGGCGCGCGCGCGCGCGCGCGCTTCCACCGGCACTCGCCCCCGCGCGCC 1349
Qy      290 ogIyThrThrLeuGlnTrpGlyAlaAlaProCysProPro-----LeuProAlaPh 307
Db      1350 CGGCACCGCAGCGGCGC--GGCGCGCGAGCTGGCGCGGACCGGCTTCGCTACGGCGCG 1406
Qy      307 eProAlaLeuLeuPro-----AlaAlaProCysArgAlaLeuLeuProLeuCyAlaTy 325
Db      1407 ACCCGCTCG--CGCGCGCGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCG-- 1463
Qy      325 rGIyAlaGlyIyLProAlaArgLeuGlyAlaArgGluAla----- 338
Db      1464 ----GCCCGGGCGCTCAGCGCTGGCGCGCTCGCCCTTCCATCGAGACATCATGGG 1519
Qy      339 -----GluValProProThrAlaProProLeuLeuLeuAl 350
Db      1520 GGAGAGCTTGGCGCGCGCGCGCGCTGGCGCGCGCGCGCGAGCGCGCGCGCTCAG 1579
Qy      350 aProLeuProAlaAlaAlaPro-----AlaIysProLeuArgGlyProAlaAlaGlyI 368
Db      1580 GCGCTCG--CGCTCGCGCTCGCGCGTGGCGCGCGCGCGCGCTCCCGGATCCCGAGAGG 1638
Qy      368 yAlaHisLeuTyCysProLeuArgLeuProAlaAlaLeuGlnAlaAlaLeu--ValArg 388
Db      1639 C-----TGGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 1668
Qy      388 rGPro--GlyProHisLeuSerTyPro 396
Db      1669 GGCGCGCGCTCACCGGATCCCTCGTGGCGG 1697

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RESULT 12  
US-10-172-118-1045

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; Sequence 1045, Application US/10172118
; Publication No. US2003022437A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yundong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999

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; CURRENT APPLICATION NUMBER: US/10/172, 118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1045
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
; DATABASE INFORMATION:
; DATABASE ACCESSION NUMBER: NM_004472
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-1045

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## Alignment Scores:

Pred. No.:	3,12e-28	Length:	2487
Score:	488.50	Matches:	170
Percent Similarity:	47.56%	Conservative:	35
Best Local Similarity:	39.44%	Mismatches:	147
Query Match:	23.01%	Indels:	83
DB:	13	Gaps:	20

US-10-087-080-32 (1-402) x US-10-172-118-1045 (1-2487)

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Qy      14 AspIysGlnGlySerAspLeuGlnGlyAlaGlyIysSerAspAlaProSerProLeuSer 33
Db      506 GAAGAGAGACACACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 564
Qy      34 AlaAlaGlyAspAspSerLeuGlySerAspGlyAspCysAlaAlaIysProSerAlaGly 53
Db      565 GCGCGCGCGCGCGCGCGCGCGCTGACCGCGGAGAGACAGCTGAGAGATCGAGAGAGA 624
Qy      54 GIGlyAlaAlaArg--AspThrGlnGlyAspGlyIyGlnSerAlaGlyIyGlyProGlyAl 73
Db      625 GAGAGACGAGATGACATCTGTG-----CTGGCGCGCGCTGTGGAGGCTCCCGCGCG 678
Qy      73 aGlnGluAlaIleProAlaAlaAlaAlaAlaAlaAlaIleGlyIyAlaGluAlaG 93
Db      679 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Qy      93 yAlaAlaGlyProGlyAlaGlyIyAlaGlySer---GlyIyGlyAlaArgSerIysPr 112
Db      721 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 777
Qy      112 cTyThrArgArgProIyProProTyTySerTyTrIleAlaLeuIleAlaMetAlaIleAr 132
Db      778 GCTGTG-----AAGCGCGCTTACTGTATATCGCTCATCATATGGCCATCTCT 828
Qy      132 gaSPSerAlaGlyIyArgLeuThrIleuAlaGluIleAsnGlyTyTrLeuMetGlyIysPh 152
Db      829 GCAGAGCCCCAGAAAGCGCTGACGCTGACGAGATCTGTGAGTTATCATACGCGCGCTT 888
Qy      829 eProPheArgGlySerTyTrIyTrIyTrArgAsnSerValArgHisAsnLeuSerIle 172
Db      889 CCCCTACTACCGGAGAGATTCCCGCGCTGGCGAGAACAGATCCGCAACTCTCGCT 948
Qy      172 uaaSPCysPheValIysValLeuArgAspProSerArgProTrpGlyIysAspAnty 192
Db      949 CAAAGACTGCTTCTCAAGATCCCCCGAGACCCGGAACCGG--GCAAGGGCAACTA 1005
Qy      192 rTtMetLeuAsnProAsnSerGlyIrrPheAlaAspGlyValPheArgArgAr 212
Db      1006 CTGGACCTGGACCGGAGTCCCGGACATGTTGACACAGCGAGCTTCTCGGCGGAG 1065
Qy      212 glyAsrGleuSerHisArgAlaProValProAlaProGlyLeuArgProGluAla-- 231
Db      1066 GAAGCGCTTCAAG--CGGACGCGCTGCTCCACCCAGCGCGCGCGCGCGAGTCTCT 1122
Qy      232 -----ProGlyLeuProAlaAla----- 237
Db      1123 GCTGCTGCGGCGCGGAGCGGAGCGGCGCGCGCGCGCGCGCGCGCT 1182
Qy      238 ---ProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArgI 256

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Db 1290 CGCGCCAGCGCGCGCGCGCGCGCGCTTCACCCGCACTGCGCCCGCGCGCC 1349  
QY 290 oGlyThrThrLeuGlnTrpGlyAlaAlaProCysProPro-----LeuProAlaPh 307  
Db 1350 CGCCACCGCAGCGCGC---GGCGCGCAGCTGGCGCGCGACCGCTTCGCTACCGCGCGC 1406  
QY 307 eProAlaLeuLeuPro-----AlaAlaProCysArgAlaLeuLeuProLeuCysAla 325  
Db 1407 ACCCGCTCG-GCGCGCGCGCTACCGCGCGCGCGCGCGCGCTTCGCGCGCGCGCGCG 1463  
QY 325 rGlyAlaGlyGluProAlaArgLeuGlyAlaArgAla----- 338  
Db 1464 ----GCCCGCGCGCTCAGCGCTGCGCGCGCTCGCTTCACGAGAGCATCATCGGG 1519  
QY 339 -----GluValProProThrAlaProProLeuLeuAl 350  
Db 1520 GCGAGCTTGGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCTCGAG 1579  
QY 350 aProLeuProAlaAlaAlaPro-----AlaCysProLeuArgGlyProAlaAlaGly 368  
Db 1580 GCGCTCG-CCCTCGCGCTCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1638  
QY 368 yAlaAlaLeuTyrcysProLeuArgLeuProAlaAlaLeuGlnAlaAlaLeu-ValArg 388  
Db 1639 C-----TCG 1668  
QY 388 rGPro---GlyProHisLeuSerTyrrPro 396  
Db 1669 GGCGCGCGCTCAGCCCGATCCCTCGTGGCGG 1697

## RESULT 14

US-09-968-007A-802  
; Sequence 802, Application US/09968007A  
; Publication No. US20040115625A1  
; GENERAL INFORMATION:  
; APPLICANT: Eber, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sigma  
; FILE REFERENCE: 689290-71  
; CURRENT APPLICATION NUMBER: US/09/968, 007A  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,172  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,173  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,278  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,294  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,295  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,316  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 1001  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 802  
; LENGTH: 5181  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-968-007A-802

## Alignment Scores:

Pred. No.: 6.16e-28 Length: 5181  
Score: 488.50 Matches: 170  
Percent Similarity: 47.56% Conservative: 35  
Best Local Similarity: 39.44% Mismatches: 147  
Query Match: 23.01% Indels: 83  
Gaps: 20

US-10-087-080-32 (1-402) x US-09-968-007A-802 (1-5181)

QY 14 AsplysGlnGlySerAspLeuGlnGlyAlaGlyGlySerAspAlaProSerProLeuSer 33

Db 2779 GAAGAGAGAGACAGACAGAGGCGCGGTCGCGCGCGC-CCGCTGCTGCTCTCCCGCGCA 2837  
QY 34 AlaAlaGlyAspAspSerLeuGlySerAspGlyAspCysAlaAlaAlaProSerAlaGly 53  
Db 2838 GCGCGCGCGCGCGCGCGCTCGACCGCGCGGAGAGAGAGCTGAGATCTGAGAGAGGA 2897  
QY 54 GylGlyAlaArg-AspThrGlnGlyAspGlyGlnGlnSerAlaGlyGlyGlyProGlyAl 73  
Db 2898 GAGAGAGAGAGATGATCTG-----CTGCGCGCGCTGCTGCGCGCGCTCCCGCGCG 2951  
QY 73 aGlnGlnAlaLeuProAlaAlaAlaAlaAlaValAlaGlnGlyAlaGlnAlaGly 93  
Db 2952 CCGCGCGCGCGCGCGCGCGCGCGCA-----GAGCGCGTGGGG 2993  
QY 93 yAlaAlaGlyProGlyAlaGlyGlyAlaGlySer---GlyGlnGlyAlaArgSerTyrr 112  
Db 2994 CG 3050  
QY 112 oTyrrThrArgArgProTyrrProProTyrrSerTyrrAlaLeuLeuAlaMetAlaLeu 132  
Db 3051 GCTGCTG-----AAGCGCGCTTACTGTTATGCGCTCATCATCTATGCGCATCT 3101  
QY 132 gAspSerAlaGlyGlyArgLeuThrLeuAlaGlnLeuGlnGlnGlnGlnGlnGlnGln 152  
Db 3102 GCAGAGCGCCAGAGAGCGCTGACGCTGAGCGAGATCTGATTCATCATCGCGCGCTT 3161  
QY 152 eProPhePheAlaGlySerTyrrThrGlyThrArgAsnSerValArgHisAsnLeuSer 172  
Db 3162 CCGCTACTACCGGAGAGAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3221  
QY 172 uAsnAspCysPheValLeuArgAspProSerArgProTrpGlyAspAsnTyrr 192  
Db 3222 CAGAGCTGCTTGTATAGATCCCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3278  
QY 192 rTrpMetLeuAsnProAsnSerGlnTyrrThrPheAlaAspGlyValPheArgArgArg 212  
Db 3279 CTGAGAGCTGAGACCGGAGATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3338  
QY 212 GlySerAlaGlySerHisArgAlaProValProAlaProGlyLeuArgProGlnGlnAla 231  
Db 3339 GAAGCGCTTCAAG---CGCGAGCGCTGCTCCCGCGCGCGCGCGCGCGCGCGCGCT 3395  
QY 232 -----ProGlyLeuProAlaAla----- 237  
Db 3396 GCTGCTCGCT 3455  
QY 238 ---ProProProAlaProAlaAlaProAlaSerProArgMetArgSerProAlaArg 256  
Db 3456 CTTCGCT 3511  
QY 256 nGlnGlnArgAlaSerProAlaGlyLysPheSerSerPheAlaAlaAspSerLeu 276  
Db 3512 GCGGCTACGCGCTGAGCTGCG-----GCTTACGCGCGCGCTCGCGCTTCTT 3562  
QY 276 uArgLysProPheArgSerArgArg-----LeuArgAspThrAlaPr 290  
Db 3563 CG 3622  
QY 290 oGlyThrThrLeuGlnTrpGlyAlaAlaProCysProPro-----LeuProAlaPh 307  
Db 3623 CGCGACCGCAGCGCGC---GGCGCGCAGCTGCGCGCGCGCGCGCTTCGCTACCGCGCG 3679  
QY 307 eProAlaLeuLeuPro-----AlaAlaProCysArgAlaLeuLeuProLeuCysAla 325  
Db 3680 ACCCGCTCG-GCGCGCGCTACCGCGCGCGCGCGCGCGCTTCGCGCGCGCGCGCG 3736  
QY 325 rGlyAlaGlyGluProAlaArgLeuGlyAlaArgAla----- 338  
Db 3737 ----GCCCGCGCGCTCAGCGCTGCGCGCTGCGCTTCATTCAGAGCATCATCGGG 3792  
QY 339 -----GluValProProThrAlaProProLeuLeuAl 350

Db 3793 GGCAGCTTGGGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCTCAG 3852  
 QY 350 aProLeuProAlaAlaPro-----AlaLysProLeuArgGlyProAlaAlaGlyG1 368  
 Db 3853 GCCTCG-CCCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3911  
 QY 368 yAlaHisLeuTyCySProLeuArgLeuProAlaAlaLeuGlnAlaAlaLeu-ValArgA 388  
 Db 3912 C-----TGCG 3941  
 QY 388 rGPro---GlyProHisLeuSerTyPro 396  
 Db 3942 GGCCTGCTCACCGATCCCTGTCGCG 3970

## RESULT 15

US-10-101-510-133  
 ; Sequence 133, Application US/10101510  
 ; Publication No. US20030148295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WAN, JACKSON  
 ; APPLICANT: WAN, YIXIN  
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
 ; FILE REFERENCE: 15117.0012  
 ; CURRENT APPLICATION NUMBER: US/10/101,510  
 ; PRIOR FILING DATE: 2002-03-20  
 ; PRIOR APPLICATION NUMBER: 60/276,947  
 ; NUMBER OF SEQ ID NOS: 805  
 ; SOFTWARE: Patent Ver. 2.1  
 ; SEQ ID NO 133  
 ; LENGTH: 2271  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-101-510-133

## Alignment Scores:

Pred. No.: 3,42e-28 Length: 2271  
 Score: 487.50 Matches: 177  
 Percent Similarity: 44.01% Conservative: 36  
 Best Local Similarity: 36.57% Mismatches: 137  
 Query Match: 22.96% Gaps: 139  
 DB: 15 Indels: 21

US-10-087-080-32 (1-402) x US-10-101-510-133 (1-2271)

QY 28 AlaProSerProLeuSerAlaAlaGlyAspAspSerLeuGlySerAspGly----- 44  
 Db 64 GCGCCCGCGCGCGG-CCTGCGCGCGCGGACCGCGGCTGGGGCGAGAGGAGCGCGGAGC 122  
 QY 45 -----AspCysAlaAlaLysPro----- 50  
 Db 123 CCGGCGCGCGCGATGCG 182  
 QY 51 -----SerAlaGlyGlyGlyAlaArg 57  
 Db 183 GATGTCGATGCTCTGCTGCTGCTGCGCGAGAAAGACATGACGATGAGTGAGGAGGCGG 242  
 QY 58 -AspThrGlnGly-----AspGlyGlnGlnSerAlaGlyGlyGlyProGlyAl 73  
 Db 243 GGAAGAAG 301  
 QY 73 agtGlnAlaAlaLeuProAlaAlaAlaAlaAlaAlaAlaAlaAlaGlyGlyAlaGly 93  
 Db 302 TGGCTGCTCCCG 361  
 QY 93 Y----- 93  
 Db 362 AGATGTCGAGAGAGAGAGAGAGAGAGAGAGATGATCTGTCGCGCGCGCTGTCGAGCTC 421  
 QY 94 -----AlaAlaGlyProGlyAlaGlyGlyAlaGlySerG1 105  
 Db 422 CCGGCG 481

QY 105 yGlnGlyAla-----ArgSerLysProTyThrArgArgPro-----LysPr 119  
 Db 482 CCG 541  
 QY 119 oProTySerTyThrAlaAlaLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 139  
 Db 542 GCGCTACTCGTAAATCGCGCTCATCATATGAGCCATCTGTGAGAGAGAGAGAGAGAGAG 601  
 QY 139 uThrLeuAlaGlnLeuAsnGlyTyLeuMetGlyLysPheProPhePheArgGlySerTy 159  
 Db 602 GAGCGTGAAGAGAGATCTGTGATTCATCATGAGCGCGCGCTCCCTCAACGAGCTGTGAAGT 661  
 QY 159 rThrGlyTyThrArgAsnSerValArgHisAsnLeuSerLeuAsnAspCysPheValLysVa 179  
 Db 662 CCGCGCTGCGAGAACAGCATCGGACACCTCGCTGCTCAACGAGCTGTGTGAAGT 721  
 QY 179 LLeuArgAspProSerArgProTyArgLysAspAsnTyTyTrpMetLeuAsnProAsnSe 199  
 Db 722 CCGCGCGAGCGCGCGAGACCGG--GGCAGAGGCACTATCGAGCGTGGAGCCGAGTC 778  
 QY 199 rGlnTyThrPheAlaAspGlyValPheArgArgArgGlyValGlyLeuSerHisArgAl 219  
 Db 779 CGCGGACATGTTCCAGACAGGAGCTTCCTGCGCGAGAGAGCGCTTCAG--CGGCA 835  
 QY 219 aProValProAlaProGlyLeuArgProGlnGlnAla----- 231  
 Db 836 GCGCTGCTCCACCAACGCGCGCGCGCGCGAGTCGTGCTGTCGCGCGCGCGGAGC 895  
 QY 232 -----ProGlyLeuProAlaAla-----ProProProAlaProAl 243  
 Db 896 CGCAGAGGAGCGCGCGAGACCGCGCAGCGCGCGCGCGCGCTTCCGCGCGCG--GCCCGCG 954  
 QY 243 AlaProAlaSerProArgMetArgSerProAlaArgGlnGlnGlnAlaSerProAl 263  
 Db 955 GCGCCCGCATGCTCAACGCGCTACGG--CCCTACGCGTGGCGGTACGCGCTGACAGCTGC 1011  
 QY 263 aGlyLysPheSerSerSerPheAlaAlaAspSerLeuAlaGlyLysProPheArgSerAr 283  
 Db 1012 C-----GCCTTACGCGCGCGCTCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCG 1062  
 QY 283 GArg-----LeuArgAspThrAlaProGlyTyThrLeuGlnTrpG1 297  
 Db 1063 CCGCGCGCGCTTCCACCGCGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1119  
 QY 297 yAlaAlaProCysProPro-----LeuProAlaPheProAlaLeuLeuPro----- 312  
 Db 1120 CCGCGAGCTGGCGCGAGACCGCTTCGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCTG 1178  
 QY 313 -AlaAlaProCysArgAlaLeuLeuProLeuCysAlaTyGlnAlaGlyGluProAlaAr 332  
 Db 1179 CCGCGCGCGCTGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1232  
 QY 332 rLeuGlyAlaArgGlnAla----- 338  
 Db 1233 CTGGCGCGCTGCGCTTCTTCATCGAGAGCATATGAGGAGCGAGCTTGGGCGCGCGCGCG 1292  
 QY 339 -----GluValProProThrAlaProProLeuLeuAlaProLeuProAlaAlaAlaAr 357  
 Db 1293 GCTGCGCGCGCGCGCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1351  
 QY 357 o-----AlaLysProLeuArgGlyProAlaAlaGlyGlnAlaHisLeuTyCySProLe 375  
 Db 1352 GTTGGCGCGCGCGCGAGCTCCCGAGTCCAGCGAGAGAGG----- 1391  
 QY 375 uArgLeuProAlaAlaLeuGlnAlaAlaLeu-ValArgArgPro---GlyProHisLeuS 394  
 Db 1392 -----TGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1441  
 QY 394 eTyTyPro 396  
 Db 1442 CGTGGCGG 1449

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Search completed: September 2, 2004, 18:14:19  
Job time : 611 secs

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